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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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DEFINITION
Oryza sativa chromosome 3 clone OSJNBa0027J18, \*\*\* SEQUENCING IN
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OFFICE
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ORGANISM
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EUKARYOOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Ehrhartoideae; Oryzaae; Oryza.

REFERENCE
Ehrhartoideae; Oryzaae; Oryza.

REFERENCE
1 (bases 1 to 144973)
Buell,R., Hsiao,J., Zismann,V., Moffat,K.M., Hill,J.,

Pred. No.

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                                                       ACATGAGCGGGAGCCCTACGGCGAACCAGGGGTGGGCGAGCTACCCGGCGCGCCCCG
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                                                                                                                                           ACCAGGCGCGGCGGTCGGGGTGGCGCCGCTGCGGTGGAGCGGCGACCTGGCGGCGG
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1 29894: contig of 29894 bp in length

29895 29994: gap of unknown length

70109 70208: gap of unknown length

70209 79598: contig of 9090 bp in length

70209 79598: contig of 3090 bp in length

70599 79698: gap of unknown length

70699 106423: contig of 26725 bp in length

106424 106523: gap of unknown length

106524 139726: gap of unknown length

139627 139726: gap of unknown length

139627 139726: gap of unknown length

139627 144973: contig of 5247 bp in length
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On Jan 9, 2002 this sequence version replaced gi:17530731.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 6 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gansberger, K., Burgess, S., Jarrahi, B., Shvartsbeyn, M., Brenner, M., Ciecko, A., Pai, G., Vanaken, S., Hansen, C., Utterbach, T., Feldblyum, T., Khalak, H.G., Yuan, Q., Quackenbush, J., White, O., Salzberg, S. and Fraser, C.
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/sub_species="japonica"
/db_xref="taxon:4530"
/chromosome="3"
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                                                                                                                                                                                                                                                                                                       Submitted (04-JUN-2002) The Institute for Genomic Research, 97;
Medical Center Dr. Rockville, MD 20850, USA
On Jun 4, 2002 this sequence version replaced gi:20153306.

* NOTE: This is a 'working draft' sequence. It currently
consists of 17 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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1 (bases 1 to 150928)

Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Tallon, L., Gansberger, K., Kim, M., Overton II, L., Bera, J., Tsitin, T., Krol, M., Jarrahi, B., Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S., Utterbach, T., Feldblyum, T., Yang, Q., Haas, B., Suh, B., Peterson, J., Quackenbush, J., White, O., Salzberg, S. and Fraser, C. Quackenbush, J., White, O., Salzberg, S. and Fraser, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC103550 150928 bp DNA linv oryza sativa chromosome 3 clone OSJNBa0079G12, PROGRESS ***, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-NOV-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA
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Oryza sativa
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AC103550.6 GI:21322019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buell, R
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contig of 11006 bp in length
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CGCACGGCAACGTGCAGGGCCAGAGCCCCTACT 68186
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                                                                                      TCGGGTGCGCGCAGGCCAGCTGCGCCACGGCCACGCTCACGCTCTGCCTGTACAACC 639
                                                                                                                 GCGCCGCGGGGCGCAGTGCGGCACGTACACGCAGGTGGTGTGGCGCAACACCGCCGAGG
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                            CGCACGGCAACGTGCAGGGCCAGAGCCCCTACT 672
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                                                         TCGGCTGCGCCCAGGCCACCTGCACCACCGGCGCCACGCTCACCATCTGCCTCTACAACC
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34725 c 33029 g 40330 t
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="3"
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95669: gap of unknown 1
109958: contig of 14289
110005: gap of unknown 1
124211: contig of 7470
131728: gap of unknown 1
131728: contig of 7470
131775: gap of unknown 1
131914: contig of 2139
133961: gap of unknown 1
141548: contig of 7587
141595: gap of unknown 1
141548: contig of 7587
141595: gap of unknown 1
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150928: contig of 2048
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                                                                                                                                                                                                                                                                                              Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@iias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, rel:81-298-38-7441, Fax:81-298-38-7466)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced.
                                                                                                                                                                                                            GCGGCGTCGGCGGCGGCGGGCGGCGTGAACGTGTTCCGCGGCTACGGCGGCGAG
                                          TGCGCGTTCGCGGACGTGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGGCGAGCTAC 446
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Отуzеае; Отуzа.
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Eukaryota; Viridiplantae; Streptophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (15-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Only in Database (2001) 2 (bases 1 to 110235)
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HTG; HTGS_PHASE2.
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/clone="0J1316_E06"
23562 c 24043 g
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Pred. No. 8e-13;
0; Mismatches 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-70L-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URI:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a working draft' sequence.

* NOTE: IT six is a "working draft' sequence."
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Only in Database (2002)
2 (bases 1 to 153428)
Sasaki, T., Matsumoto, T. and Katayose, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DNA, clone:OSJNBa0054K20
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                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica Cultivar="Nipponbare" | Japonica Kultivar="14 | Japonica | Japoni
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34064 c 34273 g 41
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Pred. No. 7.6e-13;
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Morris, S.W., Vernooij, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morris,S.W., Vernooij,B., Titatarn,S., Starrett,M., Thomas, Wiltse,C.C., Frederiksen,R.A., Bhandhufalck,A., Hulbert,S.
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/gene="Pr-1"
/gene="Pr-1"
/codon_start=1
/codon_start=1
/product="pathogenesis related protein-1"
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/protein_id="AAC25639.1"
/db_xref="GI:3290004"
/trans_lation="MAPRIACLIALAMAAIVVAPCTAQNSPQDYVDPHNAARADVGVG
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QYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGVFIICSYNPPGNVVGE
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/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05.7UL.2001) Takuji Sasaki, National Institute of Agrobiological Stences, Rice Genome Research Program; Kannondai 2.1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Nov 12, 2001 this sequence version replaced gi:15718430. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTNY2.0, BLASTNY2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent the identified cDNA sequences using RLASTN 2 0 vith the
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                               Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic Doctone:OSJNBa0091E23
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                                                                                                                                                                                                                               Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
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 IYVFTGTLDMDTLKVALSRVLVDYYPLAGRLRASNEHDGKLIIDCNSEGVLFAEGFLP
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corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from -21M13 to M13rev of the BAC clone. Detailed information on overlap and assembly quality together with annotation of this entry is available at
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/translation="MKPSRPTPHITLELKKPRERESASLSSSTSPPVVVTTTFAISVE
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LRPPTAGGGGGGRPRRELGGWIFSIFFFF"
Complement(join(19031. .19092,19181. .19629,19712. .19843,
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8140. .8634
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/gene="OSJNBa0091E23.1"
complement(2830 .6157)
/gene="OSJNBa0091E23.1"
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| Oin(22340. .22759.25490. .26449)

| /gene="05JNBa0091E23.5"

| join(22340. .22759.25490. .26449)

| /gene="05JNBa0091E23.5"
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/tb_xref="GI:18461272"
/tb_xref="GI:
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="1"
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yene="OSJNBA009LE23.3"

join(11408. .11439,14340. .14529)

yene="OSJNBA009LE23.3"
/product="putative benzoyltransferase"
/protein_id="BAB84471.l"
/db_xref="G1:18461275"
/translation="MEIVGECIYNNPPVLVTPSKPTPKLALYLSNLDDQRLLHFPIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDVKDSENASFLYRRRSRIASAVIIDYRCLGEPLFDSLRIYHLLDLTTLVHACLKQLI
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complement(join(19031.
20623. .20627))
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/codon_start=1
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complement(2830. .6157)
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complement(join(39777. .40698,40725. .41083))
/gene="OSJNBa0091E23.9"
complement(join(39777. .40698,40725. .41083))
/gene="OSJNBa0091E23.9"
/codon_start=1.
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DAFGAAHFLARWARAAMSEDSELAHPAVVAPCHDRALAPRCTPFLAKAFGH
DDASAVAEASSRLFAPPLSPVSVTFTAAHVARKKLYAPSASPLEQCTSFEALAAHVW
RAWVRALDPPASLFIKLLFTMGIRTLVKPELSGGCYCGNGFYLACAESTAGQLAASAP
DAARLYQETKORYDDDYVRSYIDLLEVRRGCLPDLAATFTISSLTRQGLEDIDFGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PELSAVVRHGDFFLTPVTLPPRPPPTEELRHQRELTVFDPVARRVLAKLTPPRHGNKR
AFHHNSGSFL1 PGRYGDQAASSSSFRVTMORCSTTV1 Y RASGGDPGLDMERLAVDDSS
TGAWSARPHTNTSDIDMFLFLKVKRYSAMHAPGRICWKRLRGGSPNSLVSLDAETINGF
PEVVPPPGVLLGPSYAVGDTDDGSMCLVNMEERGTMELVMLSKKKWHLRWLLGKSGC
GGRAWVLDQEQETSLTTSTEDAADMLMDYDRACRVVAVNAGVVLMCLHSFRRLNDRYI
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complement(32520. .33023)
/gene="OSJNBa0091E23.7"
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GKFGVTDLIGSLGVEEKVRAKDNPDKKIKRGSSANLVQKKNPNAPHNNNKKVKRDVKL
KATTNFKKKCKGKAKGNCFVCGKSGHWAKDCPDHNDKKSANNVISEGEGTSGYGKFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative pathogenesis-related protein precursor"
/protein_id="8AB84473.1"
/protein_id="8AB84473.1"
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/translation="MEASKLAICSLEVLAVVAATMEHCSDAQNSPQDYLSPQNAARSA
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VDEKKYYNVASNSCAAGKVCGHYTQVVWRDSTNVGCARVRCDANRGIFIICNYEPRGN
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/gene="OSJNBa0091E23.6"
join(29342. .29466,29780. .29964,30172. .30641)
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aslaraacacarlraiasswaflrrffTLHPSLLGHFATDADDESVIPTFHPARAQFD
                                                                                                                                                                            /product="similar
P0455H0310.25"
                                                                                                                                                                                                                                                                                   join(41911. .43020,44053.
/gene="OSJNBa0091823.10"
join(41911. .43020,44053.
/gene="OSJNBa0091823.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mkrkaspssfsgdpppaasptTvDsfCDDvIAEfLvRLpsvpSL
araacavkrwrrvasspaflrrfhalhpgQaQPLLGHYYYTECsSrpvpQpaQpTfSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="similar to Oryza sativa chromosome
P0455H0310.25"
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/gene="OSJNBa0091E23.8"
/note="hypothetical protein"
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/gene~"OSJNBa0091E23.8"
join(35671. .35809,36942.
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/gene="OSJNBa0091E23.7"
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/translation="MSTDGGVNGGHVGGGTGGGENDNINGGNNNNSNISFSGAFSSKP
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/protein_id="BAB84472.1"
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GCSDAAVRGGDFFLTRVDANAGWRVQDCRHGRLLFANESDLLVYDPLSRRGVSIRRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                    AFRISNLEVVASFSASEPVFQYQMPWPPVLLPTA"
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/db_xref="GI:18461279"
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/db_xref="GI:18461278"
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Illiopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                 Oryza sativa (japonica cultivar-group) clone:OJ1316_E06.
                                                                                                                                                      AP004057 110235 bp DNA Oryza sativa (japonica cultivar-group) OJ1316_E06, *** SEQUENCING IN PROGRESS
                                                                                                                    AP004057
AP004057.1 GI:15208425
                                                                                                     HTG; HTGS_PHASE2.
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/codon_start=1
/product="similar to Oryza
OSJNBa0077G22.24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(46301. .46382,47219. .47520,47540. .47896,48897. .49160,
49458. .49676,52147. .52173,53518. .53613,53723. .53776,
                                                                                                                                                                                                                                                                                                                 685
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join(46301. .46382,47219. .47520,47540. .47896,48897.
49458. .49676,52147. .52173,53518. .53613,53723. .537
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SLLSLRHRHPDQAHS
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VINPKRPSEYSFPGMQAAGRIYMKHDTTKLOYEDAGPMRPSYVILPEGVHPRSKYA
VGEAEDGGCCLVVLADAPHGTVFKVWRLETGKGSWPRAWTWELERRLPACEVIGKVOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BABB4477.1"
/db_xref="GI:18461281"
/tzanslation="MDSPAIPYGLSPPLLSLYLRNKPCYTKAVHGNERPRSIHPKRTA
EIDRVYGGSRRHDDDDVGDDVTTGGGSSLQTRRRTTARREERRAPARRGERRGELTGDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL Submitted (15-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mali:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the places is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

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Sasaki, T., Matsumoto, T. and Yamamoto, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, Wi:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of loontigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

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                                                                                                                     CAAGGCGCAGCAGGGTGGCACCGGCAGCGAGCGACGACGAGGACGAGTACCTGGC
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                                      G-----CCGCACAACCAGGCGCGCGCGCGGTGGGCGTGGCCCCGCTGCGGTGGAA 328
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Oryza sativa (japonica cultivar-group) chr
OSJNBB0054K20, *** SEQUENCING IN PROGRESS
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HTG; HTGS_PHASE2.
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Oryza sativa (japonica cultivar-group)
Dryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 151673)
Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Kim, M.M., Overton II, L.L., Bera, J.J., Tsitrin, T., Krol, M.I., Jarrahl, B.B., Jin, S.S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.S., Utterback, T.T., Feldblyum, T.V., Yang, O.Q., Haas, B.J., Suh, B.B., Deterson, J.J., Quackenbush, J., White, O., Salzberg, S.L. and Erzer, C. J., Quackenbush, J., White, O., Salzberg, S.L. and
                                                                         Submitted (08-AUG-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org on Aug 6, 2002 this sequence version replaced g1:19881800.
                                                                                                                                                                                                                                                                   Medical Center Dr. Rockville, MD 20850, USA 4 (bases 1 to 151673)
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-OCT-2001) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA 3 (bases 1 to 151673)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC097278 151673 bp DNA linear PLN 15-AUG OTYZA SATIVA Chromosome 10 BAC OSJNBa0040E17 genomic sequence,
BAC clone OSJNBa0040E17 is from Oryza sativa chromosome 10 The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                Submitted (06-AUG-2002) The I Medical Center Dr. Rockville, 5 (bases 1 to 151673)
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Direct Submission
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Oryza sativ
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                                                          Address all correspondence to:rice@tigr.org
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                                                                                                                                                                                                      The Institute for Genomic Research, ville, MD 20850, USA
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http://genemark.biology.gatech.edu/geneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge,
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E"
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AUTHORS
TITLE
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SOURCE
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nes 270; Conserv
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Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                               Oryza sativa.
                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                    AF306651.1 GI:21304632
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complement(15332..1536)
/rpt_family="\(\tilde{n}\) .15461)
/rpt_family="(\tilde{n}\) .15461)
/rpt_family="(\tilde{n}\) .16158)
/rpt_family="centromere"
complement(16567..16661)
Location/Qualifiers
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2 (bases 1 to 864)
Park,M.-Y., Moon,E. and Hwang,D.-J.
Direct Submission
Submitted (19-SEP-2000) Molecular Genetics, Natio
Agricultural Science and Technology, Seodundong,
441-707, Korea
                                                                                                                                                                                                                                                                                                                                                                                       AF306651 864 bp mRNA linear Oryza sativa pathogenesis-related protein 1 mRNA, AF306651
                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryzea.

1 (bases 1 to 864)

Park,M.-Y., Moon,B. and Hwang,D.-J.
Isolation and characterization of PR1 from rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 117.4; DB 8; Pred. No. 4.1e-06;
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AUTHORS
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OTYZA SALIVA genomic DNA complete sequence.
AL731633.1 GI:20452131
                                                                                          Oryza sativa.
Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
             Han, B., Feng, Q., Huang, Y.C., Li, Y., Zhu, J.J., Zhao, Q., Hu, X., Liu, Y.L., Mu, J., Yu, Z., Chen, L., Fan, D.L., Weng, Q.J., Zhang, L., Lu, Y.Q., Yu, S.L., Liu, X.H., Lu, T.T., Zhang, Y.J., Lu, Y., Li, C., Li, T., Zhang, Y., Hu, H., Jia, P.X., Qian, Y.M., Ying, K., Zhou, B., Chen, Z.H., Hao, P., Zhang, L., Wu, M., Zhang, R.Q., Guan, J.P., Fu, G.
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/protein_id="AAM45439.1"
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/KINSIATION="%ATSSLLVAAVLAAAMAATAQNSAQGDVIAASAVSSWVAEK
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GESPY"
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/cultivar="Hwachung"
/db_xref="taxon:4530"
74. .571
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/codon_start=1
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OSJNBb0096E05,
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 277; Conserva
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                                                                              GCTCGGCTGCGCGCGCACCTGCCGCAACGGCGTCGACACCGTCGCCGTCTGCGACTA
                                                                                                                   GGTCGGGTGCGCGAGGCCAGCTGCGCCACGGG----CGCCACGCTCACGCTCTGCCTGTA 634
                                                                                                                                                                                                                                      NOTE: This is a complete sequence. Genes were identified by a combination of several methods: Gene prediction programs including Egenesh (http://www.softberry.com/), genscan (http://ccm-081.mit.edu/GENSCAN.html), GeneMarkHMM (http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean Eddy, http://genome.wusti.edu/eddy/EnNAscan-SE)), searches of the complete sequence against NCBI none redundant protein database (nr) (ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-JUN-2002) Han Bin, National Center Chinese Academy of sciences, 500# Cao Bao Road, CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang,S.Y., Ren,S.X., Lv,G., Lin,W., Gu,W.Q., Zhu,G.F., Tu,Y.F., Wang,J., Yin,H.F., Zhang,Y., Cai,Z., Chen,J., Kang,H., Chen,X.Y., Shao,C.Y., Sun,Y., Hu,Q.P., Zhang,X.L., Zhang,W., Wang,L.J., Ding,C.W., Sheng,H.H., Gu,J.L., Chen,S.T., Ni,L., Zhu,F.H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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/variety="Nipponbare"
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/chromosome="4"
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/clone_Lib="CGIOTOSONBb"
/clone_Lib="CGIOTOSONBb"
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Pred. No. 2.6e-05;
0; Mismatches 150
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Best Local Similarity 56.6

Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-AUG-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* Whis sequence will be replaced by the submitter. This sequence as soon as it is
GGAGAAGGGCTCCTACGACTACGCCAGCAACAGCTGCGTCGGCGGCGCCCATGTGCGGCCA 8280:
                                                                                                    CGCCGGCGACTGCGCTGCGGCACTCCGATCGCAACAACTATCAGTACGGCGAGAACCT 82683
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Oryza sativa (japonica cultivar-group) (cultivar:Nipponicare, L...., clone:OJ1212_C12.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae;
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome clone:OJ1212_C12
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Sasaki,T., Matsumoto,T. and Katayose,Y.
Direct Submission
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="7"
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28384 CCCGGCGCTGTCGTGGGACGACCAACCTGGCGGCGTACGCGCAGGGCTACGCGAACCAGCG 28325
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Direct Submission

Submitted (01-AUG-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between the are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: It is a 'working draft' sequence.

* This sequence will be replaced

* the accession number will be preserved.

* Location/Qualifiers
                                         GGCCCCGCTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGGCGGGGGACGGTGGCGCAGCA 370
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group) chromosome 7 clone
071212_C12, *** SEQUENCING IN PROGRESS ***, in ordered pic
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                                                                                                                                                                                            Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:taasakigenias affrec go.jp, URL:http://rgp.dna.affrec.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACACGCAGGTGGTGGCGCAACACCGCCGAGGTCGGGTG----CGCGCAGGCCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGAAGGGCTCCTACGACTACGCCAGCAACAGCTGCGTCGGCGGCGCCCATGTGCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGGCGGCAGGGCGGGGGGGCGAGCGCAGCCCCTACGGCGCGAACCA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP005309 137275 bp DNA linear HTG 31-MAY-2002 Oryza sativa (japonica cultivar-group) chromosome 7 clone P0474G09, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Only in Database (2002)
2 (Dases 1 to 137275)
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
Submitted (29-MAY-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sasaki,T., Matsumoto,T. and Katayose,Y. Oryza sativa nipponbare(GA3) genomic DNA, clone:P0474G09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone: P0474G09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP005309.1 GI:21280359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP005309
                                                              /organism="Oryza sativa (japonica cultivar-group)'
| Cultivar="Nipponbare"
| /db_xref="taxon:39947"
| /chromosome="7"
                                          5
                                                                                                                                                                                Location/Qualifiers
                 29053 c 29750 g
                      4
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                      50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome
                        others
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KEYWORDS
SOURCE
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AC128878/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouke, J., Bovie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bovie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bovie, S., Brieva, M., Brown, E., Chacko, J., Cher, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Deuthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Denthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garzil, J.H., Garcia, A., Ganer, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamlton, K., Harris, K., Hart, M., Havlak, P., Hale, S., Hamlton, K., Homsi, F., Howard, S., Haber, J., Halyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlvson, J., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Levis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACACGCAGGTCGTGTGGCGCGACACCACCGCCGTCGGATGCGCCGTCGCCTGCAA 120497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGGCGGCAGGCGGGGCGGACGCGGACCGGAACCA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCGGCGCTGTCGTGGGACAACCTGGCGGCGTACGCGCAACCAGCG 120737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCCCCTACTAGCTAGC 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCCACGGCGCCACGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCA 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTACACGCAGGTGGTGTGGCGCAACACCGCCGAGGTCGGGTG----CGCGCAGGCCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGCCGTACTACCTACC 120419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCCAACCGAGGCGTCTTCTTCATCTGCACCTACTTCCCCGGCCAACGTCCAAAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGAAGGGCTCCTACGACTACGCCAGCAACAGCTGCGTCGGCGGCGCCCATGTGCGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC128878
AC128878.2 GI:22038229
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC128878 172838 bp DN
Rattus norvegicus clone CH230-511P16,
***, 55 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norway rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 172838)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 3.1e-05;
0; Mismatches 181;
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	COMMENT	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL
runs of N, but the exact sizes of the gaps are unknown.  *This record will be updated with the finished sequence *as soon as it is available and the accession number will *be preserved.  1128 1227: gap of 1127 bp in length 1228 2910: contig of 1683 bp in length *2911 3010: gap of unknown length *3011 4361: contig of 1351 bp in length *462 5971: contig of 1351 bp in length *5972 6071: gap of unknown length be preserved.  7286 6072 7285: contig of 1214 bp in length 7386 8693: contig of 1308 bp in length 8694 8793: gap of unknown length 10216: contig of 1308 bp in length 10216: contig of 1308 bp in length 10216: contig of 1423 bp in length 10216: gap of unknown length 10216: gap of unknown length 10217 10316: gap of unknown length	Submitted (02-AlG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 1, 2002 this sequence version replaced gi:21953102.  Center: Baylor College of Medicine Center code: BCM  Web site: http://www.hgsc.bcm.tmc.edu/ Contact: bqsc-help@bcm.tmc.edu/ Contact: plasc-help@bcm.tmc.edu/ Center clone name: CH230-511P16  Center project name: KAXI Center clone name: CH230-511P16  Center clone name: CH230-511P16  Center project name: Fig Dye: 100% of reads Sequencing vector: plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 117283 bases at least Q40 Consensus quality: 1172934 bases at least Q30  * NOTE: Estimated insert size may differ from sequence length  * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).  * consists of 55 contigs. The true order of the places  * arbitrary. Gaps batwen the contigs are represented as	Lozado, R.J., Lu, X., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabhat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Moser, M., Neal, D., Newtson, J., Neytson, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sudergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Tansey, J., Taylor, C., Taylor, T., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Tamerisa, A., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R. Direct Submission L. Unpublished 2 (bases 1 to 172838) Springt Ed. (24, 7015-202) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA School, C., College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
**************************************	* * * * * * * * * * * * * * * * * * *	10317 12127 1227 123411 13411 15483 15483 15483 15483 15483 15483 15483 16493 16493
object gap of unknown 73521: contig of 264 72621: gap of unknown 74779: contig of 2158 74779: contig of 4013 78992: gap of unknown 74779: contig of 4013 78992: gap of unknown 87020: contig of 383 87120: gap of unknown 90872: contig of 3752 90972: gap of unknown 93397: contig of 3752 93497: gap of unknown 93391: contig of 1894 95491: gap of unknown 93391: contig of 3430	3/20s; contig 39305; gap of 39811; contig 39811; contig 42028; contig 42028; contig 43700; gap of 46877; gap of 46877; contig 49143; contig 49243; gap of 50897; contig 50897; gap of 53147; gap of 53147; gap of 531882; contig 58728; contig 58728; contig 60365; gap of 60365; gap of 60365; gap of 63599; gap of	12126: contig of 1810 b 12226; gap of unknown l 13510: gap of unknown l 13510: gap of unknown l 13520: gap of unknown l 15882: contig of 1872 b 15482: gap of unknown l 17296: contig of 1814 b 17296: gap of unknown l 18901: contig of 1175 b 20176: gap of unknown l 20176: contig of 1175 b 20276: gap of unknown l 20176: contig of 1034 b 21210: contig of 1034 b 21210: contig of 1034 b 21210: contig of 1035 b 22410: gap of unknown l 21310: contig of 1295 b 22400: gap of unknown l 22105: contig of 1599 b 24504: gap of unknown l 26132: contig of 1628 b 26233: gap of unknown l 26132: contig of 1895 b 26233: gap of unknown l 26357: gap of unknown l 26357: gap of unknown l 30552: gap of unknown l 30573: gap of unknown l

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Search completed: March 18, 2003, 15:14:28 Job time: 3824 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            23606 GGGGAGGGG 23598
                                                                                                                                                                                                                                402 GTGGGGCCAGCCCCTACGGCGCAACCAGGGGTGGGCGAGCTACCGCGCGCCCCCCC 461
                                                                                                                522 GCCGCGGGG 530
                                                                                                                                                                                        462 GAGGTGGTGGCGTTGGGTGGCGGAGGGGCGGTACTACACCCACGCCAACAACACGTGC 521
                                                                                                                                                                                                                                                                                                                                                                                                            282 CACAACCAGCGCGCGGCGGTGGGCGTGGCCCCCGCTGCGAACGCGGGCCTGGCT 341
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99022
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1136840
1142132
1142132
1142132
1142132
1150887
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104293: contig of 5272 bp in length
104393: gap of unknown length
108459: contig of 4066 bp in length
108459: gap of unknown length
113545: contig of 4986 bp in length
113645: gap of unknown length
117970: contig of 4325 bp in length
118070: gap of unknown length
122690: contig of 4620 bp in length
122790: gap of unknown length
127723: gap of unknown length
127723: gap of unknown length
136739: contig of 4833 bp in length
136839: gap of unknown length
142131: contig of 5292 bp in length
142131: gap of unknown length
150986: contig of 8755 bp in length
151088: gap of unknown length
151088: gap of unknown length
160415: contig of 9329 bp in length
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein
   Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
BG
   318
308.5
307.5
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length: 2000000000
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Gapop 10.0 ,
  Query
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Listing
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pir2:*
pir3:*
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  Match 100%
first 45 summaries
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A24620
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T02055
A33155
S37166
S14990
S14990
B24620
S10205
S22231
T049531
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S324627
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1084.183 Million cell updates/sec
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Compugen Ltd.
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                        pathogenesis relat
pathogenesis-relat
pathogenesis-relat
                   gene PR-1
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                  protein
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S65052
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                                                                                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol. 30, 171-176, 1996
A;Title: Molecular analysis of a pistil-specific gene expressed A;Reference number: S65052; MUID:96197407; PMID:8616234
A;Accession: S65052
                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-214 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                          Matches
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
167	171.5	191.5	197	234	242	242	243	246	249.5	256.5	257	257.5	260	260.5	261.5
15.4	15.8	17.6	18.2	21.6	22.3	22.3	22.4	22.7	23.0	23.6	23.7	23.7	24.0	24.0	24.1
204	81	177	160	162	177	168	161	176	161	210	161	175	177	164	174
2	N	N	Ν	N	N	Ν	N	N	N	N	Ν	N	Ν	N	N
S27448	A05264	D84583	D85077	A96537	T08126	T07146	в96537	F84583	T52399	T04233	E85354	S43894	S04728	T04299	S71554
Sc7 protein - brac	pathogenesis-relat	probable pathogene	probable pathogene	hypothetical prote	pathogenesis-relat	pathogenesis-relat	hypothetical prote	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	PR-1-like protein	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat	pathogenesis-relat

## ALIGNMENTS

1.; Ruiter, 1996

M.M.A.; Schrauwen, J.A.M.;

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pathogenesis related protein-1 - maize C;Species: Zea mays (maize) (C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 11-May-2000 C;Accession: T02054 (Protein 26-Feb-1999) #text_change 11-May-2000 (Prot
                                                          A;Title: Induced resistance
A;Reference number: Z14524;
A;Accession: T02054
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: sts14 C;Superfamily: pathogenesis related leaf protein
                                                                                                                                                                                                                             Plant Microbe Interact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AEKKFYNYENNSCTGDDKCGVYTQIVWKKSIELGCAQRTCYEGPATLTVCFYNPPGNVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 EKPY 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 GVAPLRWNAGIASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYR-ARPAEVVALWV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 LLFFQFLLLTTASSLTHISAQTVPPPPPPPPTSA----ATPPSRAAQEFLDAHNKARSEV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVGPLTWSPMLAKETSLLVRYQRDKQNCSFANLSNGKYGGNQLWASGTVVTPRMAVDSWV
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                                                                                                   responses in maize.
MUID:98313983; PMID:9650297
                                                                                                                                                                                                                  ; Titatarn, S.; Starrett, 11, 643-658, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Mismatches
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Pred. No. 7.8
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1.8e-22;
75;
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                                                                                                                                                                                                                                                                      S.; Wiltse,
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pathogenesis-related protein 1 - maize
C;Species: Zea mays (maize)
C;Date: 08-Mar-1991 #sequence_revision 08-Mar-1991
C;Accession: A33155
R;Gillikin, J: Burkhart, W.; Graham, J.S.
submitted to the Protein Sequence Database, Februar
A;Reference number: A33155
A;Accession: A33155
A;Accession: A33155
A;Accession: A33155
A;Residues: preliminary
A;Molecule type: protein
A;Residues: 1-140 <GIL>
C;Superfamily: pathogenesis-related leaf protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Genetics:
A;Gene: PR-1
C:Superfamily: pathogenesis-related leaf protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-163 <MOR>
A;Cross-references: EMBL:U82200; NID:g3290003; PIDN:AAC25629.1; PID:g3290004
submitted to the EMBL Data Library, A;Description: Purification characte A;Reference number: S37186 A;Accession: S37166 A;Status: preliminary
                                                                                          pathogenesis-related protein 1a - barley
N;Alternate names: pathogenesis-related protein Hv-1a
C;Species: Hordeum vulgare (barley)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C;Accession: S37166
R;Bryngelsson, T.; Sommer-Knudsen, J.; Gregersen, P.L.; Collinge, D.B.; Ek,
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A33155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                               GADWSASDAVGSWVSEKQYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQGQSPY 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCKLIHSG-GPYGENLFWGSAGADWSASDAVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVGESPY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWVSEKQYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGVFIICSYNPPGN
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73; Conserv
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                                                                                             Sommer-Knudsen, J.; Gregersen, P.L.; Collinge, D.B.; Ek, B.;
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                                                                characterization
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Pred. No. 8.3e-
                                                                               September 1993
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                                                            and molecular cloning of
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A;Molecule type: mRNA
A;Residues: 1-164 <BRY>
A;Cross-references: EMBL:X74939; NID:g401830; PIDN:CAA52893.1; PID:g401831
C;Superfamily: pathogenesis-related leaf protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogenesis-related protein T16L1.220 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 11-Jun-1999
R:Casacuberta, J.M.; Puigdomenech, P.; San Segundo, B. Plant Mol. Biol. 16, 527-536, 1991
A;Title: A gene coding for a basic pathogenesis-related A;Reference number: S14969; MUID:91329688; PMID:1714315 A;Accession: S14969
                                                                                              pathogenesis-related protein - maize
C;Specites: Zea mays (maize)
C;Date: 13-Jan-1995 #sequence_revisi
C;Accession: S14969
                                                                                                                                                                            RESULT
S14969
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C; Superfamily: pathogenesis-related leaf protein
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A; Residues: 1-172 <BEV>
A; Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T04990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: cultivar Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                         QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAVSWSTKL-QAYAQSYANQ-RIGDCKLQHSG-GPYGENIFWGSAGADWKAADAVKLWVD 101
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                                                                                                                                                                                                                                                                                                 GATLTLCLYNPHGNVQGQSPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN 122
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                                                                                                                     #sequence_revision
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41.0%;
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Pred. No. 5.5e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 307.5; DB 2;
Pred. No. 6.9e-18;
9; Mismatches 56;
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vember 1998
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A;Experimental source: Nicotiana tabacum cv. Samsun NN after inoculation with R;Ohabhima, M.; Harada, N.; Matsuoka, M.; Ohashi, Y.

Nucleic Acids Res. 18, 181, 1990

A;Title: The nuclotide sequence of pathogenesis-related (PR) 1b protein gene A;Reference number: S07579; MUID:90174914; PMID:2308824

A;Accession: S07579

A;Status: translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathogenesis related protein 1b precursor - common tobacco C:Species: Nicotiana tabacum (common tobacco) C:Date: 30-un-1988 *sequence_revision 30-Jun-1988 *text_change 2 C:Accession: B24620; S07579; S02223; S08588 R:Cornelissen, B.J.C.; Hooft van Huljsduijnen, R.A.M.; Van Loon, EMBO J. 5, 37-40, 1986 A;Title: Molecular characterization of messenger RNAs for 'pathog A;Reference number: A24620 A;Accession: B24620
A;Cross-references: EMBL:X12486; NID:g19947; PIDN:CAA31009.1; PID:g19948 R;Payne, G.; Parks, T.D.; Burkhart, W.; Dincher, S.; Ahl, P.; Metraux, J.; Plant Mol. Biol. 11, 89-94, 1988 A;Title: Isolation of the genomic clone for pathogenesis-related protein A;Reference number: $04032 A;Reference number: $04032 A;Recession: $06858 A;Molecule type: protein A;Recidues: 94-110;148-153;158-168 <PAY>C;Superfamily: pathogenesis-related leaf protein C;Keywords: pyroglutamic acid F:1-30/Domain: signal sequence #status predicted <SIG>F;31-180/Product: pathogenesis-related protein lb #status predicted <MAT>F;31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #s
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A;Molecule type: DNA
A;Residues: 1-167 - CCAS>
A;Cross-references: EMBL:X54325; NID:g22453; PIDN:CAA38223.1; PID:g22454
C;Superfamily: pathogenesis-related leaf protein
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A; Residues: 1-168 <COR>
A; Cross-references: EMBL: X03465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X17680; R;Cutt, J.R.; Dixon, D.C.; Carr, Carr, Cucleic Acids Res. 16, 9861, 1988
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A; Residues: 'A', 17-168 < CUT>
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A; Residues: 1-168 < OHS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATG-ATLTLCLYNPHGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVGVGPVTWSTKLQQFAEKYAAQ--RAGDCRLQHSG-GPYGENIFWGSAGFDWKAVDAVR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGW--ASYRARPAEVVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVILLWIVMAAATAVHPSY--------SENSPQDYLTPQNSARA 43
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J.P.; Klessig, D.F.
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Pred. No. 1.3e-17;
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Metraux, J.P.;
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RESULT
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                                                                                                                                                                                                                                                  pathogenesis-related protein 1b - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 13-Jan-195 #sequence_revision 13-Jan-1995 C;Accession: S22531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X52555; NID:g20055; PIDN:CAA36790.1; A;Experimental source: cv. Wisconsin 38 C;Superfamily: pathogenesis-related leaf protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Nucleotide sequences of two PR-1 pseudogenes from A; Reference number: S10205; MUID:90287728; PMID:2356132 A; Accession: S10205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogenesis-related protein 1 - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 C;Accession: $10205
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                                                     A;Gene: prb-1b
C;Superfamily:
                                                                                                                          A; Molecule type: DNA
A; Residues: 1-179 < EYA>
                                                                                                                                                                             R;Eyal, Y.; Sagee, O.; Fluhr, R.
Plant Mol. Biol. 19, 589-599, 1992
A;Title: Dark induced accumulation of a basic pathogenesis-related
A;Reference number: S22531; MUID:92329719; PMID:1627772
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A; Residues: 1-184 <PFI>
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                                                                                                          A; Cross-references:
                                                                                                                                                               A; Accession: S22531
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Best Local
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Best Local 9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NQGWASYR-ARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAQASCATGATLTLCLXNPHGNVQGQSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPYGAN--QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA---- 116
                                                                                                                                                                                                                                                                                                                                                                                                     NSGGYVVSCNYDPPGNFVGQSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGATLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAQNSPQDYLDAHNTARADVGVEPLTWDDQVAAYAQNYASQ--LAADCMLVH-SHGQYGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHAQNSQQDYLDAHNTARADVGVEPLTWDNGVAAYAQNYVSQ-----LAADCNLVHSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLAWGSGDFMTAAKAVEMWVNEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARAQC
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                                                     pathogenesis-related leaf protein
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                                                                                                          EMBL: X66942;
27.9%;
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                                                                                                        NID: g19969;
Pred. No.
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Pred. No. 1.4e-17;
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Pred. No. 1.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                       168
   Score 302.5;
Pred. No. 1.
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 8e-17
                   DВ
               2,
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               Length
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                     179;
                                                                                                          PID:g19970
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Local

l Similarity 62; Conserv

Conservative

17;

Mismatches

61;

Indels

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Gaps

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pathogenesis-related protein 1c precursor - common tobacco C; Species: Nicotiana tabacum (common tobacco C; Species: Nicotiana tabacum (common tobacco) C; Date: 30 - Jun - 1988 #sequence_revision 01-Dec-1995 #text_ch C; Accession: $07580; C24620; S01705 R; Ohshima, M.; Harada, N.; Matsuoka, M.; Ohashi, Y. Nucleic Acids Res. 18, 182, 1990 A; Title: The nucleotide sequence of pathogenesis-related (FA; Reference number: $07580; MUID:90174915; PMID:2308825 A; Accession: $07580 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Map position: 4
A:Mote: T16I1.210
C:Superfamily: pathogenesis-related leaf protein
C:Superfamily: pathogenesis-related protein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-163/Product: pathogenesis-related protein 1, 19.3K #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
T04989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathogenesis-related protein 1 precursor, 19.3K - Arabidopsis thaliana N;Alternate names: protein TiGL1.210 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000 C;Accession: T04989; S71271 B;Bevan, M; Obermaler, B; Deutschenbaur, S; Piravandi, E; Hohelsel, J.; submitted to the Protein Sequence Database, November 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; molecule type: DNA
A; Residues: 1-77,'p',79-82,'L',84-88,'RL',91-92,'RR',95-162,'LLKENSI'
A;Cross-references: EMBL:X96600; NID:g1228948; PID:g1228950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kloska, S.; Schuster, W.
submitted to the EMBL Data Library,
A;Reference number S71271
A;Accession: S71271
                                                                                                                                                                                                                                                                                                           В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-163 <BEV>
A; Cross-references: EMBL: AL031394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: Z15393
A; Accession: T04989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANOGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC
                                                                                                                                                                                                                                                                                                           CNYDPPGNWVGEWPY
                                                                                                                                                                                                                                                                                                                                                                                      SMTGVAAVDMWVDEQFDYDYDSNTCAWDKQCGHYTQVVWRNSERLGCAKVRCNNGQTFIT 148
                                                                                                                                                                                                                                                                                                                                                                                                              RARPAEVVALWVAEGRYYTHANNTCAAGROCGTYTOVVWRNTAEVGCAQASCATGATLTL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFLAVHNRARAEVGVGPLRWDEKVAAYARNYANQ--RKGDCAMKHSSGS-YGENIAWSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGSNATADEXLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.4%;
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Pred. No. 4.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 March 1996
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A;Map position: 4
A;Note: T16L1.201
A;Note: T16L1.201
C:Superfamily: pathogenesis-related leaf protein
F;1-27/Domain: signal sequence #status predicted
F;28-166/Product: pathogenesis-related protein 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;ACCESSION.
A;ANOICCULE type: DNA
A;Residues: 1-166 <KLO>
A;Cross-references: EMBL:X96600; NID:g1228948; PIDN:CAA65419.1; PID:g1228949
A;Cross-references: EMBL:X96600; PID:g1228948; PID:g1228949
A;Cross-references: EMBL:X96600; PID:g1228948; PID:g1228949
A;Cross-references: EMBL:X96600; PID:g1228949
A;Cro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kloska, S.; Schuster, W. submitted to the EMBL Data A;Reference number: S71270 A;Accession: S71270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the Protein Sequence Database, A; Reference number: Z15393
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R;Cutt, J.R.; Dixon, D.C.; Carr,
Nucleic Acids Res. 16, 9861, 1988
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A;Residues: 1-168 < OHS>
A;Cross-references: EMBL:X17681; NID:g19957; PIDN:CAA35666.1; PID:g19958
R;Cornelissen, B.J.C.; Hooft van Huijsduijnen, R.A.M.; Van Loon, L.C.; BC
EMBO J. 5, 37-40, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-166 <BEV>
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A; Residues: 6-168 < CUT>
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A; Residues: 1-130 <COR>
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A; Accession: C24620
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62; Conser
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pathogenesis-related protein precursor - barley C;Species: Hordeum vulgare (barley) C;Decies: Hordeum vulgare (barley) C;Date: 14-Jul-1995 *sequence_revision 21-Jul-1995 *text_change 20-Aug-1999 C;Accession: $52627; S37188 R;Mouradov, A.; Mouradova, E.; Scott, K.J. Plant Mol. Biol. 26, 503-507, 1994 A;Title: Gene family encoding basic pathogenesis-related 1 proteins in barley. A;Reference number: $52626; MUID:95036024; PMID:7524728 A;Accession: $52627 A;Molecule type: mRNA A;Residues: 1-164 <MOU>A;Cross-references: EMBL:226320; NID:9402210; PIDN:CAA81229.1; PID:9402211 C;Superfamily: pathogenesis-related leaf protein F:1-24/Domain: signal sequence *status predicted <SIG>F;25-164/Product: pathogenesis-related protein *status predicted <MAT>
                        pathogenesis-related protein 1 precursor - barley C. Species: Hordeum vulgare (barley) C. Species: Hordeum vulgare (barley) C. Species: Hordeum vulgare (barley) C. Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change C. Accession: S39474; S32002 R. Muradov, A.; Petrasovits, L.; Davidson, A.; Scott, K.J. Plant Mol. Biol. 23, 439-442, 1993 A.; Title: A cDNA clone for a pathogenesis-related protein 1 from A. Reference number: S39474; MUID:94033324; PMID:8219079 A.; Mccession: S39474 MUID:94033324; PMID:8219079 A.; Mccession: S39474 A.; Molecule type: mRNA A.; Molecule type: mRNA A.; Mesidues: 1-164 <MURD: A.; Molecule type: mRNA A.; Molecule type: mRNA A.; Molecule type: mRNA A.; Molecules: 1-164 <MURD: MURD: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNVRGRRPY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKKDYNYGSNTCAAGKYCGHYTQVVWRASTSIGCARVVCNNNRGVFIT-CNYEPRGNIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT - - GATLTLCLYNPHGNVQG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAILLALAMAAAMVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHARDDVSVPHIKWHAG-AARYAWNYAQRRKRDCRLIHSNSRGRYGENLAWSSGDMSGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVRLWVREKSDYFHKSNTCRAGKQCGHYTQVVWKNSEWVGCAKVKCDNGGTFVTCNYSHP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRARPAE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
EMBL: Z21494; NID: g22760; PIDN: CAA79703.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.8%;
39.1%;
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9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 290.5;
Pred. No. 1.6
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   PID: g22761
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                                                                                                                                                               barley
                                                                                                                                                                                                                                                                                            20-Aug-1999
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pathogenesis-related protein 1 precursor, 17.6K - Arabidopsis thaliana C;Species; Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change 16-Feb-2001 C;Accession: JQ1693; PQ0471; C84519 C;Accession: JQ1693; PQ0471; C84519 C;Ribers, S.; Mauch-Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch-Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch-Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch-Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch-Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch-Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch-Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch-Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Mauch-Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Milliams, S.; Dincher, Mani, B.; Moyer, M.; Potter, S.; Williams, S.; Dincher, R;Uknes, S.; Milliams, S.; Milliams, S.; Dincher, R;Uknes, S.; Milliams, S.; Dincher, M;Uknes, S.; Milliams, S.; Milliams, S.; M;Uknes, S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: pathogenesis-related leaf protein F;1-26/Domain: signal sequence #status predicted · F;27-161/Product: pathogenesis-related protein 1,
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A; Title: Acquired resistance in Arabidopsis
A; Reference number: JQ1693; MUID:93005717;
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F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-164/Product: pathogenesis-related protein 1 #status predicted <MAT>
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A; Residues: 42-67;104-112;153-161 < UXN1>
A; Experimental source: leaf
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A; Residues: 1-161 <STO>
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A; Residues: 1-161 <UKN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: At2g14610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M90508; NID:g166860;
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                                                                                                                                                                                 VLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGYAPLRWNAGLASAAAGTVA 101
EQLR-GNCRLIHSG-GPYGENLAWGSGDLSGVSAVNMWVSEKANYNYAANTC--NGVCGH
                                                                 QQRRQGGCAFADVGASPYGANQGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGT 161
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38.6%; Pre-
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39.5%;
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                                                                                                                                           --SPQDYLRVHNQARGAVGVGPMQWDERVA-AYARSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID: g3810599; PIDN: AAC69381.1;
                                                                                                                                                                                                                                                                          Score 288; DB 2; Pred. No. 2.4e-16; Score 288; DB 2; Pred. No. 2.4e-16; Score 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 288.5;
Pred. No. 2.3
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, 17.6K #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                    Length 161;
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Search completed: March 19, 2003, 09:36:05 Job time : 19 secs	Qy 162 Db 120 Search con Job time	162 YTQVVWRNTAEVGCAQASCATGATLTLCLYNPHGNVQGQSPY 203         : :    :       :       :	61
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Maximum Match 100%
Listing first 45 summaries
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  357.5
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Gapop 10.0 , Gapext 0.5
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1085
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 SwissProt_40:*
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 PRO4_LYCES
PRO5_LYCES
PROBLYCES
PRI_MEDTR
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YOHB_YEAST
YM9_YEAST
YM5_VESVI
AEGI_MOUSE
YR81_CAEELI
VA3_SOLIN
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Q41495 solanum tub
Q00008 zea mays (m
p07053 nicotiana t
p09042 nicotiana t
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p040374 medicago tr
p11670 nicotiana t
Q08697 lycopersico
p35794 schizophyll
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p47032 saccharomyc
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Q0340 mus musculu
Q09566 caenorhabdi
p35785 vespula pen
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45	44	43	42	41	40	39	38	37	36	35	3 <b>4</b>
105.5	107.5	110	110	110.5	111	112	112	113	113.5	114.5	115
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## ALIGNMENTS

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01-DEC-1992 (Rel. 2
01-DEC-1992 (Rel. 2
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement.
                                                                                                                         Interpro; IPR001283; Allrgn_V5/Tpx1.
pfam; pF00188; SCP; 1.
PRINTS; pR00837; V5TPXLIKE.
ProDom; pD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A gene coding for a basic pathogenesis-related (PR-like) per from Zea mays. Molecular cloning and induction by a fungus moniliforme) in germinating maize seeds.";
Plant Mol. Biol. 16:527-536(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. W64A; TISSUE=Seed;
MEDLINE=91329688; PubMed=1714315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnollophyt Panicoideae; Andropogoneae; NCBI_TaxID=4577;
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
Plant defense; Pathogenesis-related protein; SIGNAL 1 27
CHAIN 28 167 PATHOGENESIS-REL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- function: probably involved in the defense reaction of against pathogens.
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                                                                                                                                                                                                                                                     MaizeDB; 66057;
                                                                                                                                                                                                                                                                                  HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDUCTION: BY FUNGAL INFECTION IN GERMINATING SEISIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMA INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEGRYYTHANNTCAAGROCGTYTOVVWRNTAEVGCAQASCATG-ATLTLCLYNPHGNVQG
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                                                                                                                                                                                                                                                                                                         S14969; S14969.
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                                                                                                                                                                                                                                                                                  P04284; 1CFE.
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                                                                                                                                                                                                                                                                                                                                                                       s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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RESULT 3
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                                                                                                                                                                                        MEDLINE=89041576; PubMed=3186451;
Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.;
"Isolation and nucleotide sequence of cDNA clones
pathogenesis-related proteins PRIa, PRIb and PRIc
tabacum cv. Xanthi nc induced by TMV infection.";
Nucleic Acids Res. 16:9861-9861(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of tobacco."
                      proteins to the extracellular space idioblasts.";
                                                                    MEDLINE=91224081; PubMed=2026137; Dixon D.C., Cutt J.R., Klessig D.F.; "Differential targeting of the tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                            related' proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Samsun N
Cornelissen B.J.C.,
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153
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EMBL; X03465; CAA27183.1; ...
EMBL; X12486; CAA31009.1; ...
EMBL; X17680; CAA35665.1; ...
EMBL; X17680; B24620.
PIR; $07579; $07579.
HSSP; P04284; 1CFE.
                                                                                                                                                                                                       PRIC_TOBAC STANDARD; PRT; 168 AA.

P09042;
01-NOV-1988 (Rel. 09, Created)
11-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis-related protein 1C precursor (PR-1C).
Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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PROSITE; PS01009; SCP_AG5_PR1_SC7_1;
PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
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pfam; pF00188; SCC; 1.
pr1NTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               + +
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SEQUENCE FROM N.A.
STRAIN-cv. Samsun NN; TISSUE-Leaf;
MEDLINE-90174915; PubMed-2308875;
Ohshima M., Harada N., Matsuoka M.
                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; casteridae; euasterids I; Solanales; Solanaceae; NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.

INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER CONTROL OF THE PATHOGEN INFECTION OR OTHER CONTROL OR OTHER CONTROL OF THE PATHOGEN INFECTION OR OTHER CONTROL OR OTHER CONTROL OF THE PATHOGEN INFECTION OR OTHER CONTROL OR OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQYGENLAQGSGDFMT-AAKAVEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVG
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16
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     Matsuoka M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 304; DB 1;
Pred. No. 2.3e-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203
     Ohashi Y.;
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                                                                                                                                                                                     core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001283; Allrgn_V5/Tpx1.
pfam; pF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X17681; CAA35666.1; -.
EMBL; X05454; CAA29023.1; -.
EMBL; X12487; CAA31010.1; -.
PIR; S07580; S07580.
HSSP; P04284; LCFE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The nucleotide sequence of pathogenesis-related (PR) 1c of tobacco.";
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1. PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1. Plant_defense; Pathogenesis related proplant_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91224081; PubMed=2026137;
Dixon D.C., Cutt J.R., Klessig D.F.;
"Differential targeting of the tobacco
proteins to the extracellular space and
idioblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfitzner U.M., Goodman H.M.;
"Isolation and characterization of cDNA clones encoding pathogenesi
related proteins from tobacco mosaic virus infected tobacco plants.
Nucleic Acids Res. 15:4449-4465(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-89041576; PubMeCutt J.R., Dixon D.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 18:182-182(1990)
[2]
SEQUENCE OF 6-168 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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MEDLINE=87231027;
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Nucleic Acids Res. 16:9861-9861(1988).
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                         125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: PROBABLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELATED RESPONSES
WASYR-ARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATG
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                                                                                                                               EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGANQG 124
                                                                               DYLDAHNTARADVGVEPLTWDDQVAAYAQNYASQ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10:1317-1324(1991)
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                        31
168 AA;
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D.D., Carr J.P., Klessig D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=3295779;
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18583 MW;
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                                                                                                                                                                                        15;
                                                                                                                                                                                                                                        Score 296;
                                                                                                                                                                                                              Pred. No.
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                                                                               -----LAADCNLVHSHGQYGENLA
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                                                                                                                                                                                                                                                                                           CRC64;
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01-JUN-1994
15-JUN-2002
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PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                               PIR; S37188; S37188.
HSSP; P04284: 10PP
                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pathogenesis-related protein PRB1-2 precursor.
Hordeum vulgare (Barley).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Dales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HORVU
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P35792;
                                                                                                                                                SEQUENCE
                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                    PROSITE; PS01009; SCP_AG5_PRI_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PRI_SC7_2; 1.
Plant defense; Pathogenesis related protein; Signal; Multigene family.
SIGNAL BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                     EMBL; Z26320; CAA81229.1;
                                                                                                                                                                                                                                                                                                                                                                                                           between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        barley."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouradov A., Mouradova E., Scott K.J.; "Gene family encoding basic pathogenesis-related 1 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. PSAKNON RESISTANT; TIS
MEDLINE=95036024; PubMed=7524728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO A FAMILY INSECTS AG3/AG5; FUNGI SC7/SC14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PROBABLY INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAINST PATHOGENS
                                                                                   LATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYIVSCNYDPPGNVIGKSPY 168
                        GAVSWSTKL-QAFAQNYANQ-RINDCKLQHSG-GPYGENIFWGSAGADWKAADAVNSWVN 101
                                          APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATLTLCLYNPHGNVQGQSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WGSGDFLTAAKAVEMWVNEKQYYAHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MO1. Biol. 26:503-507(1994).
                                                                                                                 Similarity
                                                                                                                                               68
113
135
164 AA;
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                                                                                                        Conservative
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25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29, Created)
29, Last sequence update)
41, Last annotation update
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119
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25
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                 Pred.
                                                                                                                           Score 290.5;
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PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Leaf;
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                                                                                                                                               DDB722DB74EFE390 CRC64;
                                                                -LSQAQN--
                                                                                                        Mismatches
                                                                                                                 ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                      THAT GROUPS MAMMALIAN SCP/TPX1; AND PLANTS PR-1.
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                                                                                                                          DB 1;
                                                                                                       61;
                                                               SPODYVSPHNAARSAVGV
                                                                                                        Indels
                                                                                                                         Length 164;
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                                                                                                      Gaps
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PIR; S39474; S39474.
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                              ProDom;
                                                                                                                                                                                                                                                                                  InterPro; IPR001283; Allrgn_V5/Tpx1
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                     EMBL; Z21494; CAA79703.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: PROBABLY INVOLVED AGAINST PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94033324; PubMed=8219079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSPY 203
                                                      LAILLALAMAAAMVN-----
                                                                                                                                                                                                                                                 ; PR00837; V5TPXLIKE; PD000542; Allrgn_V5/Tpx1; SM00198; SCP; 1.
                                                                                            Similarity
71; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hordeum.
                                                                                                                                       164 AA;
                                                                                              Conservative
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119
150
17683
                                                                                                        26.6%;
38.6%;
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                                                                                              24;
                                                                                             Pred. No. 3.6
; Mismatches
                                                                                                        Score 288.5;
Pred. No. 3.
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EGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT--GATLTLCLYNPHGNVQG
EKKDYNYGSNTCAAGKVCGHYTQVVWRASTSIGCARVVCNNNRGVFIT-CNYEPRGNIVG
     160
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2092 (Rel. 41, Last annotation update)
15-JUN-2092 (Rel. 41, Last annotation update)
Pathogenesis-related protein 1 precursor.
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its Muradov A., Petrasovits L., Davidson A., Scott K.J.;
"A cDNA clone for a pathogenesis related protein 1 from barley.";
Plant Mol. Biol. 23:439-442(1933)
-i- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

PROSITE; PS01009; SCP\_AG5\_PR1\_SC7\_1; 1.
PROSITE; PS01010; SCP\_AG5\_PR1\_SC7\_2; 1.
PROSITE; PS0101010; SCP\_AG5\_PR1\_SC7\_2; 1.
PATHOGENES; Pathogenesis-related protein; Signal; Multigene SIGNAL 1 24 BY SIMILARITY.
CHAIN 25 164 PATHOGENESIS-RELATED PROTEIN 1.
PATHOGENESIS-RELATED PROTEIN 1. BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY. PATHOGENESIS-RELATED PROTEIN 1. PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY). 80972FF654F77395 CRC64;

24 LATLIALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGV -----LSQAQN-----.6e-16; les 60; -SPQDYVSPHNAARSAVGV Indels 29; Gaps 83 44

Length

164;

8

GAVSWSTKL-QAFAQNYANQ-RINDCKLQHSG-GPYGENIFWGSAGADWKASDAVNSWVS APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVA 141 101

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PRESULT AND DESCRIPTION OF THE PROPERTY OF THE
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                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Eujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Wolfat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Rongeman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI_RRATH STANDARD; PRT; 161 AA. P33154; 01-OCT-1993 (Rel. 27, Created) 01-OCT-1993 (Rel. 27, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Pathogenesis-related protein 1 precursor (PR-1). AT2G14610 OR T6B13.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions the Duropean Bioinformatics Institute and the EMBL outst the European Bioinformatics Institute. There are no restrictions the Duropean Bioinformatics institutions as long as its content is in
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InterPro; IPR001283; Allrgn_V5/Tpx1.
pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                        EMBL; M90508; AAA32863.1; -.
EMBL; AC005398; AAC69381.1;
PIR; JQ1693; JQ1693.
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 402:761-768(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20083487; PubMed=10617197;
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SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNCI SC7/SC14 AND PLANTS PR-1.
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Matches 64
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PROSITE; PS01010; S
Plant defense; Sigr
SIGNAL 1
CHAIN 27
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[2]
NEMLINE-CV. Address.

MEDILINE-809/41576; PubMed-3186451;

Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.;

"Isolation and nucleotide sequence of cDNA clones for the nathogenesis-related proteins PRIA, PRIb and PRIC of Nicol
                                                                                                                                                                         STRAIN-cv. Wisconsin 38; Pfitzner U.M., Pfitzner A.J.P., Goodman H.M.; Pfitzner A.J.P., Goodman H.M.; "DNA sequence analysis of a PR-la gene from tobacco: relationship of heat shock and pathogen responses in Mol. Gen. Genet. 211:290-295(1988).
                                                                                                                                                                                                                                                                                                                                                  STRAIN-cv. Samsun NN;
MEDLINB-88083595; Pubbed-3691804;
MEDLINB-88083595; Pubbed-3691804;
Ohshima M., Matsuoka M., Yamamoto N., Tanaka Y., Ka
Ozeki Y., Kato A., Harada N., Ohashi Y.;
"Nucleotide sequence of the PR-1 gene of Nicotiana
FEBS Lett. 225:243-246(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; edicotyledons; core eu
Asteridae; euasterids I; Solanales; Solanaceae; Nicot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Samsun NN;
MEDLINE=88015528; PubMed=3658669;
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                                                                                                                                    SEQUENCE OF 4-168 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cornelissen B.J.C., Horowitz J., van Kan J.A.L., Goldberg R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Structure of tobacco from the PR-1 group.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e PR-1 group.";
Acids Res. 15:6799-6811(1987).
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161 AA;
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SCP_AG5_PR1_SC7_2; 1.
gnal; Pathogenesis-related
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Kano-Murakami
             of Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                 tabacum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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Nucleic
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ProDom; PD000542; Allrgn_V5/Tpx1;
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PIR; A05264; A05264.
HSSP; P04284; ICFE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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EMBO J. 4:2745-2749(1985).
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                                                                                                                                                                                                                                                             Plant defense;
                                                                                                                                                                                                                                                                         PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
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                                                                         LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV
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  GVEPLTWDDQVAAYAQNYASQ----
                         GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV
                                                 LLVSTLLLFLVI--
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Acids Res.
                                                                                                             Similarity
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                                                                                                  Conservative
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                                                                                                                                                  18573 MW;
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36.7%;
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LF >> VS (IN REF. 4).

D -> S (IN REF. 5).

SQ -> PS (IN REF. 3).

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Y -> W (IN REF. 5).
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-> W (IN REF. 5).
27375217031292E0 CRC64;
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EMBL; 226332; CAA81234.1; -.
EMBL; X264940; CAA52894.1; -.
PIR; S37189; S37189.
PIR; S37209; S37209.
PIR; S37209; S37209.
PIR; S37167; S37167.
HSSP; P04284; ICEE.
DISULFID DISULFID
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                   pfam; pF00188; SCP; 1.
pRINTS; PR00837; V5TPXLIKE.
proDom; PD000542; Allrgn_V5/Tpx1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "purification, characterization, and molecular cloning type pathogenesis related proteins from barley."; mol. Plant Microbe Interact. 7:267-275(1994).
-i- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bryngelsson T., Sommer-Knudsen J., Ek B., Thordal-Christensen H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Pallas; TISSUE=Leaf; MEDLINE=94281675; PubMed=8012045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pathogenesis-related protein PRB1-3 precursor (PR-1B) (HV-8).
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Psaknon resistant, and cv.
MEDLINE=95036024; PubMed=7524728;
Mouradov A., Mouradova E., Scott K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994
15-JUN-2002
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                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol.
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                                         MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196
                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAINST PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLTLCLXNPHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NYRGESPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVQGQSPY 203
                                                                                  defense;
                                                                                                                                                                              IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation updat
  68
113
                                       09; SCP_AG5_PR1_SC7_1; 1.

10; SCP_AG5_PR1_SC7_2; 1.

Pathogenesis-related protein; Signal; Multigene family.

1 BY SIMILARITY.

5 164 PATHOGENESIS-RELATED PROTEIN PRB1-3.

5 25 PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26:503-507(1994)
  140
119
(BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gregersen P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REACTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collinge D.B.
                                                                                                                                                                                                                                                                                                                                                             restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLANTS
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PRESCRIPTOR RESIDENT CONTROL OF THE 
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    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAMNI
                                                       DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI_SAMNI STANDARD; PRT; 167 AA.
041359;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis related protein PR-1 type precursor.
Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coupe S.A., Taylor J.E., Roberts J.A.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF
AGAINST PATHOGENS.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                            Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                 EMBL; Z46947; CAA87071.1; -.
HSSP; P04284; 1CFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                  CHAIN
                                                                                                                                SIGNAL
                                                                                                                                                       Plant defense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Abscission zone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 PRGNIVGQKPY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVALWVAEGRYYTHANNTCAAGROCGTYTQVVWRNTAEVGCAQASCAT--GATLTLCLYN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MQTPKLVILLALAMSAAMV------NLSQAQN-----SPQDYVSPHNA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATACLLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARAAVGVGAVSWSTKL-QAFAQNYANQ-RINDCKLQHSG-GPYGENIFWGSAGADWKASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                     PS01009; SCP_AG5_PR1_SC7_1; 1. PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135
164 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                30
72
                                                   Pathogenesis-related protein; Signal.

1 29 POTENTIAL.

1 7 PATHOGENESIS-RELATED PROTEIN PR-1 TYPE.

2 144 BY SIMILARITY.

3 123 BY SIMILARITY.

BY SIMILARITY.

9 153 BY SIMILARITY.
                                      ΑA;
                                                                                                                                                                                                                          Allrgn_V5/Tpx1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 I
17697 MW;
                                      18410 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.3%;
    26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 285.5;
Pred. No. 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
  Score 283.5;
                                      4F2BAB3269592E53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DA4B279B9F5C50C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 164;
Length 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCP/TPX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
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  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
PR04_LYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 57; Conserv
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PRO4_LYCES STANDARD; PRT; 159 AA.

Q04108;
Q04108;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis-related leaf protein 4 precursor (P4).
Lycopersicon esculentum (Tomato).
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS010101; SCP_AG5_PR1_SC7_2; 1
PROSITE; PS010101; SCP_AG5_PR1_SC7_2; 1
Plant defense; Pathogenesis related protein; Signal; Multigene family.
SIGNAL 1 24 BY SIMILARITY.
CHAIN 25 159 PATHOGENESIS BEATED LEAF PROTEIN 4.
POTROSITE CARBOYFLIC ACID
MOD_RES 25 25 PYRROLIDONE CARBOYFLIC ACID
DISULFID 68 136 BY SIMILARITY.
                                                                                                                                                                                                                           Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    van Kan J.A.L., Joosten M.H.A.J., Wagemakers C.A.M., van den Berg-Velthuis G.C.M., de Wit P.J.G.M., "Differential accumulation of mRNAs encoding extracellular and intracellular PR proteins in tomato induced by virulent and avirulent races of Cladosporium fulvum.", "Plant Mol. Biol. 20:513:527(1992).
                                                                                                                                                                                                                                                                                                                                                                      EMBL; M69247; AAA03615.1;
EMBL; A22634; CAA01613.1;
HSSP; P04284; 1CFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Moneymaker; TISSUE=Leaf; MEDLINE=93043041; PubMed=1421154;
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001283; Allrgn_V5/Tpx1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDUCTION: UPON INFECTION BY VIRILENT AND AVIRLLENT RACES OF PATHOGENS, FOR EXAMPLE FUNGAL PATHOGEN C.FULVUM. SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION FOUND DURING AND DAYS 8 TO 12 AFTER INOCULATION WITH AN AVIRULENT VIRULENT PATHOGEN RESPECTIVELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAINST PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCNYSPPGNYAGQRPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLT 187
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5; Mismatches
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DISULFID
SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-CV. MILL; TISSUE-Leaf;
STRAIN-C-04151430; PubMed-8108502;
Conejero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P04284; Q04109;
20-MAR-1987 (Rel. 04, Created)
01-JUN-1994 (Rel. 29, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Pathogenesis-related leaf protein 6 pr
protein P1) (P14) (P14A) (PR protein).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-cv. VFN8; TISSUE-Leaf;
MEDLINE=97348583; PubMed-9204567;
MEDLINE=97348583; Conejero V.,
Tornero P., Gadea J., Conejero V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYCES
                                                                                                                                                                                                                                              "Two PR-1 genes from tomato are differentially regulated and reveal novel mode of expression for a pathogenesis-related gene during the hypersensitive response and development.";
Mol. Plant Microbe Interact. 10:624-634(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-cv. Moneymaker; TISSUE-Leaf; MEDLINE-93043041; PubMed-1421154;
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                                                                                                                           Lucas J., Camacho Henriquez Sanger H.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tornero P., Rodrigo T., Conejero V., Vera P.;
"Nucleotide sequence of a cDNA encoding a pathogenesis-related protein, pl-pl4, from tomato (Lycopersicon esculentum).";
Plant Physiol. 102:325-325(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Mol. [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van Kan J.A.L., Joosten M.H.A.J., Wagemakers C.A.M., van den Berg-Velthuis G.C.M., de Wit P.J.G.M.; or "Differential accumulation of mRNAs encoding extracellular and intracellular PR proteins in tomato induced by virulent and avaces of Cladosporium fulvum.";
                                                     unfamiliar
                                                                        "Amino acid sequence of the
from viroid-infected tomato
                                                                                                                                                                                                SEQUENCE OF 25-159.
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| SYRARPAEVYALMVABGRYYTHANNYCAAGROCGTYTQVVWRIASVRLGCGRARCUNGWWF 142
| SYRARPAEVYALMVABROCVGGKWCGHYTQVVWRISVRLGCGRARCUNGWWF 142
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61; Conserv
                        iar proteins.";
4:2745-2749(1985)
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Viridiplantae; Strepto
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                                                                  'pathogenesis-related' leaf protein reveals a new type of structurally
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Pred. No. 1.2e-15;
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                                                                                                                                                                                                                                                                                                                                              Vera P.;
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MOD_RES
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PIR; S26239; S26239.
PIR; S29628; S29628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1: FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS AGAINST PAYHOGENS. HAS ANTIFUNGAL ACTIVITY.

-!- DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION FOUND DURING DAYS 4 TO AND DAYS 8 TO 12 AFFER INOCULATION WITH AN AVIRULENT AND A VIRULENT PATHOGEN RESPECTIVELY.

VIRULENT PATHOGEN RESPECTION BY VIRULENT AND AVIRULENT RACES OF PATHOGENS, FOR EXAMPLE FUNGAL PATHOGEN C.FULVUM. ALSO INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "NMR solution structure of the pathogenesis-related protein P14a.";
J. Mol. Biol. 266:576-593(1997).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
Plant defense; Pathogenesis~related pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 1CFE; 12-NOV-97.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
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Wuethrich K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR. MEDLINE=97220236; PubMed=9067611;
                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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                                                                                                                                                                                                                                                        69
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SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSECTS AG3/AG5;
                                                                                                                                                                                                                                             EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN--QGWA 126
                                                                                                               ISCNYDPVGNWIGQRPY 159
                                                                                                                                         TLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                              DYLAVHNDARAQVGVGPMSWDANLASRAQNYA -- NSRAGDCNLIHSGA -- -
                                                                                                                                                                                                 SYRARPAEVVALWYAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATL 186
                                                                                                                                                                      DFTGRAA--VQLWVSERPSYNYATNQCVGGKKCRHYTQVVWRNSVRLGCGRARCNNGWWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M69248; AAA03616.1; -. X68738; CAA48672.1; -. Y08804; CAA70042.1; -.
                                                                                                                                                                                                                                                                                   l Similarity
61; Conser
                                                                                                                                                                                                                                                                                                                                          25
25
68
109
131
123
159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3D-structure.
                                                                                                                                                                                                                                                                                   Conservative
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      159
136
136
115
145
                                                                                                                                                                                                                                                                                                25.6%;
                                                                                                                                                                                                                                                                                                                                          17520 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGS TO A FAMILY THAT GROUPS MAMM FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                   Score 277.5;
Pred. No. 2.6e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                          MISSING (IN REF. 4).
; EA35A6C3AC0EF3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                PATHOGENESIS - RELATED LEAF PROTEIN PYRROLIDONE CARBOXYLIC ACID.
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Signal; Multigene family;
                                          173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ramage P., Moesinger
                                                                                                                                                                                                                                                                                   .6e-15;
es 54;
                                          Ā
                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAMMALIAN
                                                                                                                                                                                                                                                                                                             Length 159;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                              -GENLAKGGG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCP/TPX1;
                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                   Gaps
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RESULT 14
PRB1_TOBAC
ID PRB1_
AC P1165
DT 01-00
DT 01-00
DT 15-JJ
DE Basic
OS Nicot
OC Eukan
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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PRBI_TOBAC STANDARD; PRT; 177 AA.

P11670;
P11670;
O1-OCT-1989 (Rel. 12, Created)
O1-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Basic form of pathogenesis-related protein 1 precursor (PRP 1).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
                                                                                                                                                                                                                                                                                                                                                                  DISULFID DISULFID DISULFID
                                                                                                     TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001283; Allrgn_V5/Tpx1.
pfam; pF00188; SCP; 1.
pRINTS; pR00837; V5TPXLIKE.
proDom; pp000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
Plant defense; Pathogenesis related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago truncatula (Barrel medic).

Bukaryota; Viridiplantue; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosic

eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicag
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X79778; CAA56174.1; -. HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Physiol. 107:273-274(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  truncatula.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Szybiak-Strozycka U., Lescure N., Cullimore J.V., Gamas P.;
"A cDNA encoding a PR-1-like protein in the model legume Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95175606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Pathogenesis-related
                                                                                                                                                      151
                                                                                                                                                                              182
                                                                                                                                                                                                                             123
                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                      91
                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAINST PATHOGENS
                                                                                                                                                      DDKGTFMTCNYDPPGNYYGERPY
                                                                                                                                                                                                   IFWGSGVGWNPAQAVSAWVDEKQFYNYWHNSCVDGEMCGHYTQVVWGSTTKVGCASVVCS
                                                                                                                                                                             TG-ATLTLCLYNPHGNVQGQSPY
                                                                                                                                                                                                                          QGWAS-YRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCA 181
                                                                                                                                                                                                                                                     SRSFKNQFLIPQNIARAAVGLRPLVWDDKLTHYAQ-WYANQRR-NDCAL-EHSNGPYGEN 90
                                                                                                                                                                                                                                                                             SNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN 122
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=7870819;
                                                                                                                                                                                                                                                                                                                                                      19760 MW;
                                                                                                                                                                                                                                                                                                                 24.7%;
42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein PR-1 precursor.
                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                               Score 268.5;
Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.

PATHOGENESIS-RELATED PROTEIN PR-1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                      173
                                                                                                                                                                              203
                                                                                                                                                                                                                                                                                                                                                      898B00C9CD72DE4A CRC64;
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                 .4e-1
                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                             Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago.
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PR1A_LYCES
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Best Local S
Matches 57
PRIA_LYCES STANDARD; PRT; 175 AA.

Q08697;
Q10-007-1996 (Rel. 34, Created)
Q1-0CT-1996 (Rel. 34, Last sequence update)
Q1-0CT-1996 (Rel. 34, Last sequence update)
Q1-0CT-1996 (Rel. 34, Last annotation update)
Q1-0CT-1996 (Rel. 34, Last annotation update)
Q1-0CT-1996 (Rel. 34, Last annotation update)
Q2-0CT-1996 (Rel. 34, Last annotation update)
Q2-0CT-1996 (Rel. 34, Created)
Q2-0CT-1996 (Rel. 34, Cre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carnes M., Ryals J.;
"Isolation and sequence of a genomic clone encepathogenesis related protein 1 from Nicotiana Plant Mol. Biol. 12:595-596(1989).
-i- FUNCTION: PROBABLY INVOLVED IN THE DEFENSI AGAINST PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant defense; Pathogenesis-related protein; Multigene family; Signal.
SIGNAL 1 23 BY SIMILARITY.
CHAIN 24 177 BASIC FORM OF PATHOGENESIS-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00198; SCP; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
Probom; PD000542; Allrgn_V5/Tpx1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X14065; CAA32228.1;
PIR; S04728; S04728.
HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-cv. Xanthi;
Payne G., Middlesteadt W., Desai N., Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ANQGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 NNGWFFITCNYDPPGNFIGQRPF 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SGSNATADEYLAPHNQARAAYGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: TWO DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGATLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKAQNSPQDYLNPHNAARRQVGVGPMTWDNRLAAYAQNYANQ--RIGDCGMIH-SHGPYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENLAAAFPQLNAAGAVKMWVDEKRFYDYNSNSCVGG-VCGHYTQVVWRNSVRLGCARVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĀΑ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 6.767; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3DA58AF784C206E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN THE DEFENSE REACTION OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tabacum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotiana
                                                 eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACID
                                                                               Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ß
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SEQUENCE FROM N.A.
STRAIN-CV. Rutgers;
STRAIN-Q4247356;
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MEDLING-94247356; PubMed-8190070;
Tornero P., Conejero V., Vera P.;
Tornero P., Conejero V., Vera P.;
"A gene encoding a novel isoform of the PR-1 protein family from tomato is induced upon viroid infection.";
Mol. Gene Genet. 243.47-53(1994).
-i- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
AGAINST PATHOGENS (BY SIMILARITY).
-i- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
RELATED RESPONSES.
-i- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3.AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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6: sp_mammal:*
7: sp_mhc:*
10: sp_phage:*
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## ALIGNMENTS

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1 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
1 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
2 Similarity to pathogenesis-related protein (Unknown protein)
3 Similarity to pathogenesis-related protein (Unknown protein)
4 (Hypothetical 20.1 kda protein)
5 (Hypothetical 20.1 kda protein)
6 (Hypothetical 20.1 kda protein)
7 (NKIF13.27 OR ATGS66590.
8 KATAJIA 27 OR ATGS66590.
9 KATAJIA 27 OR ATGS66590.

                                                                                                                                                                  SEQUENCE FROM N.A.

Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,

Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Palm C.J., Bowser L., Jones T., Banh J., Kamiya A., Kawai J.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P. K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned P1 and TAC clones."; DNA Res. 5:203-216(1998).
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MEDLINE-98403884; PubMed-9734815;
MAKAMURA Y., Sato S., Asamizu E.,
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen I Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A.,
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Best Local Similarity
Matches 69; Conserv
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Wiltse C.C., Frederiksen R.A., Bhandhufalck A., Hu
"Induced resistance responses in maize.";
MOL. Plant Microbe Interact. 11:643-658(1998).
EMBL; U82200; AAC25629.1; -.
EMBL; U82200; AAC25629.1; -.
HSSP; P04284; ICFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PP00188; SCP; 1.
PFINTS; PR00037; V5TPXLIKE.
ProDom; PD000342; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
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EMBL; AB013389; BAB10935.1; -.

EMBL; AF386987; AAK62432.1; -.

EMBL; AY093248; AAM13247.1; -.
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SMART; SM00198; SCP; 1.
Hypothetical protein.
SEQUENCE 185 AA; 20099 MW; A2F91
                                                                                                                PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.

SEQUENCE 163 AA; 17224 MW; 8331850F13365219
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NCBI_TaxID=4577;
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ACLLALAMAAIVVAPC --
                                                        Similarity 39. 73; Conservative
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"Polymorphism of PR-1-like proteins
Preeding Sci. 46:293-293(1996).
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Tomimoto Y., Ikehashi H., Kakeda K.,
"A pistil-specific PR-1 like protein
sequence and genealogical position.",
Breeding Sci. 49:97-104(1999).
EMBL, AB015047; BAA34937.1; -
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Theaceae; Camellia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                              InterPro; IPR001283; Allrgn_V5/Tpx1.
pfam; PF00188; SCP; 1.
proDom; PD000542; Allrgn_V5/Tpx1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomimoto Y.,
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                   ProDom; PD00054; SMART; SM00198;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-PISTIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Camellia sinensis (Tea).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR-1 like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157
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 178
                        191
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                                                                                                                 75
                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVGESPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGN 196
                      YNPH-GNVQGQSPY 203
                                                                   AEVVALWVAEG-RYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCA-TGATLTLCL
                                                                                           NSARAEVGVDPLKWSYSLANAASRLVRYQKNYMHCEFADMTGQLQYGSNQMWSDYSAKPP
                                                                                                         NQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADV-GASPYGANQGWASYRAR-P
                                                                                                                                         ILPVLLLVIC -- HSSTHLLADHPIAARWVPPG--
                                                                                                                                                               LLLATLLALCAAPAPTH-----GARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQGQSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWYSEKQYYDHDINSCAEGQYCGHYTQYVWRDSTAIGCARVYCDNNAGYFIICSYNPPGN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCKLIHSG-GPYGENLFWGSAGADWSASDAVG
YYPHPGNLGGQRPY
                                             REVVEYWVNSGKKHYRYTHNYCVRNQNCGPYKQVVWEKTEMVGCAQGVCGNNNGSLSICF
                                                                                                                                                                                      Similarity
75; Conserv
                                                                                                                                                                                                                                 1
191 AA;
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamaguchi S.,
                                                                                                                                                                                                                                                                    SCP;
                                                                                                                                                                                                                                                                    Allrgn_V5/Tpx1;
CP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor.
  191
                                                                                                                                                                                                                                 36 P
21591 MW;
                                                                                                                                                                                                 30.0%;
38.7%;
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10,
21,
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                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                               Score 325.5; DB 1
Pred. No. 3.7e-17;
                                                                                                                                                                                                                                 POTENTIAL. 6764CEA8CBF80467 CRC64;
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  detected
                                                                                                                                                                                                                                                                                                                                                              Kowyama Y.;
of Camellia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191
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                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                      61;
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                                                                                                                                          -----AARQFVDAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikehashi
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                                                                                                                                                                                                          Length
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                                                                                                                                                                                                             191;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Camellia.";
                                                                                                                                                                                      33;
                                                                                                                                                                                      Gaps
                                                                      190
                                                                                            117
                                                                                                                   132
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                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
               Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                          08W084 PRELIMINARY; PRT; 167 AA.
08W084; PRELIMINARY; PRT; 167 AA.
08W084; PRELIMINARY; PRT; 167 AA.
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 21, Last amoutation update)
01-JUN-2002 (TrEMBLrel. 21, Last amoutation update)
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; pP00188; SCP; 1.
PR.NTS; PR00837; V5PPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
SMART; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
SRCQUENCE 164 AA; 18397 MW; 840F99DB9FA7DF39 CRC64;
                                                                        Putative pathogenesis-related OSJNBA0091E23.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV.
Murray J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
Submitted (JUN-1999) to the
EMBL; AF149413; AAD40121.1;
HSSP; P04284; ICFE.
            NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XH05;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T1N24.14.
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                                                                                                                                                                                                              149
                                                                                                                                                                                                                                                                                    128
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                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                              LCLYNPHGNVQGQSPY
                                                                                                                                                                                                                                                         GALSGAEAVKLWVNEKSDYIYASNTCSDGKQCGHYTQVVWRTSEWVGCAKVKCDNGGTFV
                                                                                                                                                                                                                                                                              YRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLT 187
                                                                                                                                                                                                                                                                                                      DYLDEHNRARTQVGVPPMKWHAG-AEQYAWNYAQQRK-GDCSLTHSNSNGLYGENLAWSG
                                                                                                                                                                                                                                                                                                                            EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASP-YGANQGWAS 127
                                                                                                                                                                                                             TCNYYPPGNYRGRWPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y J., Langston Y., Clarke K., Drone sequence of A. thaliana TlN24.";
                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana Genome
ed (MAY-1999) to
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      28.9%; Sco
46.3%; Pre
%ative 18;
                                                                                                                                                                                                            164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing Project.";
the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12,
12,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                    Score 313.5;
Pred. No. 2.5
                                                                                    protein.
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                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164
                                                                                                                                                                                                                                                                                                                                                                      .5e-16;
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                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
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                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                164;
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RESULT 6
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Best Local S
Matches 73
                                                                                           EMBL; X74939; CAA52893.1; -.
HSSP; P04284; 1CFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2001) to the EMBL/GenB
EMBL; AP003853; BAB84473.1; -
InterPro; IPR001288; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN=CV. PALLAS; TISSUE-LEAF;
MEDLINE-94281675; PubMed-8012045;
MEDLINE-942801 T., Sommer-Knudsen J.,
                                          Signal
SIGNAL
                                                                                                                                                                                             Bryngelsson T., Sommer-Knudsen J., Greyerson. .....

Bk B., Thordal-Christensen H.;

Purification, characterization and molecular cloning of basic PR-1-

"Purification, characterization and molecular cloning of basic PR-1-
                                                                                                                                                                                                                                                                                                                                                                        01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
PR-la pathogenesis related protein (Hv-la) precurso.
    SEQUENCE
                                                                                                                                                                                       type pathogenesis related proteins from barley Mol. Plant Microbe Interact. 7:267-275(1994).
                                                                                                                                                                                                                                                                                                                            Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Str.
Spermatophyta; Magnollophyta;
Triticeae; Hordeum.
                                                                     PROSITE;
                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q43489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki tiva nipponbare(GA3) genomic
clone:OSJNBa0091E23.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; UNKNOWN_1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.

SEQUENCE 167 AA; 18334 MW; 40AE3EA728443D2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PY -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PΥ
                                                                                E; PS01009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKYYNYASNSCAAGKVCGHYTQVVWRDSTNVGCARVRCDANRGIFIICNYEPRGNIVGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMSWSTKLQGFAEDYARQ--RKGDCRLQHSG-GPYGENIFWGSAGADWTAADAVRSWVDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVAE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASKLAICS-----LEVL-----AVVAATMEHCSDAQNSPQD-YLSPQNAARSAVGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
                                                                     PS01010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                          Hordeum.
  164
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                             25
25
  AA;
                                                                SCP_AG5_PR1_SC7_1;
SCP_AG5_PR1_SC7_2;
                          24
164
 17440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.5%;
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                                                                                                                                                                                                                                                                                                                                    Streptophyta; Er
yta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
               (HV-lA)
                         PR-1A PATHOGENESIS RELATED PROTEIN
                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 309; DB 10;
Pred. No. 5.5e-16;
1; Mismatches 68;
063F219DEFE7E548 CRC64;
                                                                  <u>. . . </u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA,
                                                                                                                                                                                                                                                                                                                                    Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                             precursor
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Best Local Similarity
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                            InterPro; IPRO01283; Allrgn_V5/Tpx1.

pfam; pF00188; SCP; 1.

praints; pR00837; V5Tpx1IKE.

proDom; pD000542; Allrgn_V5/Tpx1; 1.

SMARR; SM00198; SCP; 1.

SMARR; SM00198; SCP, AG5_PR1_SC7_1; 1.

PROSITE; pS01100; SCP_AG5_PR1_SC7_2; 1.

PROSITE; pS01100; SCP_AG5_PR1_SC7_2; 1.

SEQUENCE 172 AA; 18830 MW; 6E94C8CADAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core ev

Burosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pathogenesis-related protein - like (Pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project; submitted (MAR-2000) to the EMBL/G EMBL; AL031394; CAA20586.1; -. EMBL; AL161584; CAB80090.1; -. HSSP; P04284; LCFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obermaier B., Deutschenbaur Mayer K.F.X.; Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Obermaier B., Deutschenbaur S., Piravandi E., Hoheisel J.,
Heijnen L., Vos P., Mewes H.W., Mayer K.F.X., Schueller C.,
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T16L1.220 OR AT4G33730
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                      123
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                                                                                                                    63
                                                                                                                                                                                             Local
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                                                                                                                                                                                                                    Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC-ATGATLTLCLYNPHGNVQGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAVSWSTKL-QAYAQSYANQ-RIGDCKLQHSG-GPYGENIFWGSAGADWKAADAVKLWVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVALWVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAILLALAMAAAMVN-----LSQAQN-----SPQDYLSPHNAARAAVGV
                                                                                                SNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN 122
                    QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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41.0%; Pred. No. 5.8e-16;
tive 19; Mismatches 62
                                                                                                                                                                                             28.3%;
44.7%;
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                                                                                                                                                                                             Score 307.5; pred. No. 7.
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                                                                                                                                                                    7.3e-16;
nes 56;
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                                                                                                                                                                                                                    DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
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                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jesse T.,
Bevan M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                      Gaps
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Best Local S
Matches 63
                                                                                                   Q40597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).
Bukaryota; Viridiplantae; Stretpohyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
Tobacco W38/1 PR-1 pathogenesis related protein.
 SEQUENCE FR
STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00837; V5TPXLIKE.

ProDom; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

SEQUENCE 184 AA; 20384 MW; OFFB1BEBF4A1D565 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90287728; PubMed=2356132;
Pfitzner A.J.P., Pfitzner U.M., Goodman H.M.G.
Nucleotide sequences of two PR-1 pseudogenes
v. Wisconsin 38.";
Nucleic Acids Res. 18:3404-3404(1990).
EMBL; X52555; CAA36790.1;
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q40597;
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Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=WISCONSIN 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4097;
                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                  NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                         GAQNSPQDYLDAHNTARADVGVEPLTWDDQVAAYAQNYASQ--LAADCMLVH-SHGQYGE
                                                                                                                                                                                                                                                                                                                                       GSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATLTLCLYNPHGNVQGQSPY
                                                                                                                                                                                                                                                                         LAFGSGDMSAAQAVAMWVHEKSYYDFYSNSC-HGPACGHYTQVVWRGSARLGCGKAKCNN
                                                                                                                                                                                                                             NSGGYVVSCNYDPPGNFVGQSPY
                                                                                                                                                                                                                                                                                                                                                                      Similarity 63; Conserv
 FROM N
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                   28.0%;
44.1%;
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                                                                                                        Last sequence update)
Last annotation updat
n 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                  Score 304;
Pred. No. 1
                                                                                                                                              Created)
                                                                                                                                                                                                                                                     203
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                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                      169
                                                                                                                                                                                                                                                                                                                                                                        DB 10;
1.4e-15;
hes 59;
                                                 Arabidopsis
                                                            Embryophyta; Tracheophyta; edons; core eudicots; Rosid
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                                                                                                                       update)
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                                                               Rosidae
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULTATION OF THE STATE OF THE
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01-JUN-2002
Prb-1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q04106;
Q04106;
01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. SAMSUN;
STRAIN-CV. SAMSUN;
MEDLINE-92329719; PubMed-1627772;
Eyal Y., Sagee O., Eluhr R.;
Fyal Y., Sagee O., Eluhr R.;
"Dark-induced accumulation of a basic pathogenesis-related (PR-1)
"Dark-induced accumulation of a basic pathogenesis related (PR-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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Submitted (MAR-1996) to the
EMBL; X96600; CAA65420.1; -.
HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                              PRINTS; PRO0837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 1
                                                                                                                                                                                                                                                                                                                                                                                        PRB-1B.
Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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ProDom; PD000542; Allrgn_V5/Tpxl;
                                                                                                                                                                                           PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
SEQUENCE 179 AA; 20120 MW; 7003FF0E1755152B CRC64;
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     SQAQNSPQDYLNPHNAARRQVGVGPMTWDNRLAAFAQNYANQ~-RAGDCRMQHSG-GPYG
                                                 SGSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYG 120
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SCP_AG5_PR1_SC7_2;
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                                                                                                Score 302.5;
Pred. No. 1.8e
7; Mismatches
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Pred. No. 1.
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POTENTIAL.
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hes 61;
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Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pathogenesis-related protein 1 precursor, 19.3K (Putative pathogenesis-related protein 1 precursor protein) (T16L1.210)
(AT4G33720/T16L1_210)

***YPRI OR T16L1.210 OR AT4G33720.

***YPRI OR T16L1.210 OR AT4G33720.

***PRI OR T16L1.210 OR AT4G33720.

***PRI OR T16L1.210 OR AT4G33720.

***Examptophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheoph Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; peurosids II; Brassicales; Brassicaceae; Arabidopsis.

****YPRI OR T16L1.210 OR AT4G33720.

***Examptophyta; Magnoliophyta; Embryophyta; Tracheoph Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; peurosids II; Brassicales; Brassicaceae; Arabidopsis.

***YPRI OR T16L1.210 OR AT4G33720.
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Obermaier B., Vos P.,
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Brooks S.,
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.W., Mayer K.F.X.,
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Best Local
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Matches 73;
                  Query Match
Best Local Similarity
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082714;
01-NOV-1998 (TremBLrel. 08, C
01-NOV-1998 (TremBLrel. 21, L
01-UN-2002 (TremBLrel. 21, L
Pathogenisis-related protein
PR. 1.1.
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PROSITE; PS01009; SCP, 1.

PROSITE; PS010109; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS010101; SCP_AG5_PR1_SC7_2; 1.

SEQUENCE 163 AA; 18492 MW; F0C568A56765C76E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae; Triticeae; Noot manner man
                                                                                                                                                                                                                                                                                                            Molina A., Gorlach J., Volrath S., Ryals J.; "Wheat genes encoding two types of PR-1 proteins are pathogen-inducible, but do not respond to activators of systemic acquir
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum (Wheat).
Eukaryota; Viridiplantae;
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                                                                                                                                                                 PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                               Submitted (JUL-1998) to the EMBL; AJ007348; CAA07473.1;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                      SEQUENCE
                                                                                                                                  PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                  resistance."
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4565;
                                                                                                                                                                                                                   Pfam; PF00188; SCP;
                                                                                                                                                                                                                                                  HSSP; P04284; 1CFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00188; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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                                                                        AA:
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164
17651
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                        27.3%;
39.7%;
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          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation 1.1 precursor.
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Pred. No. 3.
        Score 296.5; DB 10
Pred. No. 4.6e-15;
9; Mismatches 63;
                                                                                       PATHOGENISIS-RELATED PROTEIN
                                                                        6D652EB2646B8A44 CRC64;
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          29;
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RESULT
Q39187
                                             Submitted (DEC-2001) to the E EMBL; X96600; CAA65419.1; ... EMBL; AL031394; CAA20584.1; ... EMBL; AL161584; CAB60088.1; -EMBL; AY070411; AAL49907.1; -HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q39187;
Q39187;
Q1-NOV-1996
                                                                                                                                                                                                     Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Che Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M. Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Spermatophyta; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pathogenesis-related protein 1 precursor (Pathogenesis-related protein 1, precursor, 18.9K) (Putative pathogenesis-related protein 1,
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Heijnen L., Vos P., Mewes H.
Submitted (AUG-1998) to the
                                                                                                                                                                                                                                                                                                                           Yamada K., Banh J.
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EU Arabidopsis seg
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Kloska S., Schuster
                                                                                                                                                                 Theologis A.;
"Full Length cDNA of gene
                                                                                                                                                                                                                                                                                                                                                                                 Submitted
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                                   InterPro;
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        Pro; IPR001283; Allrgn_V5/Tpx1.
PF00188; SCP; 1.
PR00837;
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(MAR-2000) to the EMBL/GenBank/DDBJ databases
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V5TPXLIKE
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dons; core eudicots; Rosid
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, Schueller C.,
J databases.
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M., Wu H.C.,
hen H., Cheuk R.,
                                                                                                                                                                                                                                  Seki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lemcke
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, Bevan
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RESULT 14
Q94F73
ID Q94F7
AC Q94F7
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-JU
DE Patho
OS Triti
OC Eukar
OC Sperm
OC Triti
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Matches 71
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Best Local
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SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q94F73;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pathogenesis-related protein 1.
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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SMART; SM00198; SCP; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Yu L., Niu J.-S., Ma Z.-Q., Chen P.-D., Liu D.-J.;
"Cloning and characterization of pathogenesis-related protein wheat.";
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF384143; AAK60565.1; ...
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam: PF00188; SCP; 1.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
PROSITE; PS010109; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
PROSITE; PS010109; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
SEQUENCE 164 AA; 17537 MW; 5E2605216D1F9E25 CRC64;
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102
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EKKDYDYGSNTCAAGKVCGHYTQVVWRASTSIGCARVVCNNNLGVFIT-CNYEPRGNIIG
                           EGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT--GATLTLCLYNPHGNVQG 199
                                                                                                   GAVTWSTKLQGFAQSYANQ-~RINDCKLQHSG-GPYGENIFWGSAGADWKAADAVNAWVG 101
                                                                                                                                       APLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA---RPAEVVALWVA 141
                                                                                                                                                                                                          LAILLALAMSAAMAN-
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166 POTENTIAL.
18952 MW; A32EEF66245CDC5B CRC64;
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Search completed: March 19, 2003, 09:38:11 Job time: 32 secs

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COOls H.J., Ishii H.;
"Pre-treatment with Acibenzolar-S-methyl Systemically Primes
"Phenylalanine Ammonia Lyase (PAL1) Gene Expression in Cucumber
"Phenylalanine Ammonia Lyase (PAL1)
                                                                                                                                                                                                                                                                                                                                                                                                                  Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
pathogenesis-related protein 1-la (Fragment).
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GTFIICNYEPRGNFLYQRPY
                                                                        ASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCA--TG 183
                                                                                                              DFYGYHNVARAQYGYGFIEWDKTYAS-----FAQQYANRRLNDCRLVNSG-GFYGENIAW 60
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                           ATLTLCLYNPHGNVQGQSPY
                                                        GSPDLSAKDAVQLWVDEKPFYNYETNTCAAGELCGHYTQVVWRKSVRIGCAKVRCTDNIG 120
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14; Mismatches 55
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Arabidopsis thalia
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Arabidopsis thalia
Arabidopsis thalia
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tabacum

XX

New nucleic acid encoding a pathogen-related protein isolated maize and designated PRI-C10, useful for transforming plants fenhanced disease resistance

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25-0CT-1999
25-0CT-1999
26-0CT-1999
26-0CT-1999
26-0CT-1999
28-0CT-1999
28-0CT-1999
28-0CT-1999
29-0CT-1999
                                                                                                                                                                                                                                                                                                         SAR; tobacco; protein-synthesis independent gene; cyclohexamide; systemic acquired reistance response; anti-pathogen; plant protection; maize; PR-1.
This sequence represents the maize PR-1 like protein, PR-1mz. The cDN encoding this sequence was isolated by screening a BTH-induced cDNA library was screened using a probe matching to the PR-1 barley clone HVPR1BR. The cDNA encoding this sequence,
                                                                         New DNA contg. plant systemic acquired resistance genes - and transgenic plants contg. them, impart disease and pest resistance, also Arabidopsis gene promoter to control DNA transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-1999;
22-OCT-1999;
                                                      Claim 21; Page 70-71; 85pp; English.
                                                                                                                       N-PSDB;
                                                                                                                                                      Alexander DC,
                                                                                                                                                                            (CIBA ) CIBA
                                                                                                                                                                                                 13-JAN-1994;
                                                                                                                                                                                                                     03-JAN-1995;
                                                                                                                                                                                                                                            20-JUL-1995
                                                                                                                                                                                                                                                                 WO9519443-A2
                                                                                                                                                                                                                                                                                     Zea mays.
                                                                                                                                                                                                                                                                                                                                                    PR-1 like protein PR-1mz
                                                                                                                                                                                                                                                                                                                                                                            20-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                    AAR91595 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 NATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQ 123
                                                                                                                      1995-263872/34.
DB; AAQ99804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KESTVLTICFYNPPGNIIGQKPY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GWAS--YRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAT-LTLCLYNPHGNVQGQSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LWAKGLVAVTPSLAVETWVKEKPFYNYKSDTCAANHTCGVYKQVVWRNSKELGCAQATCT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAAAKAFTDAHNKARAMVGVPPLVWSQTLEAAASRLARYQRNQKKCEFASLNPGKYGANQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                            GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990S-0161404.

990S-0161405.

990S-0161359.

990S-0161361.

990S-0161361.

990S-0161361.

990S-0161920.

990S-0161993.

990S-0161993.
                                                                                                                                                     Ryals JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0160815.
99US-0160980.
99US-0160981.
                                                                                                                                                                                                 94US-0181271
                                                                                                                                                                                                                      95WO-IB00002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99us-0160989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.0%;
47.6%;
                                                                                                                                                      Uknes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                     163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 347.5;
Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                      SJ,
                                                                                                                                                      Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .9e-24
                                                                                                                                                      ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
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Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY29944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ99800-Q99803 and AAQ99805 are all used in recombinant/chimaeric DNA molecules of the invention. The DNA sequences were isolated by differential screening of a cDNA library, followed by analysis by Northern hybridisation to RNA in the presence and absence of cyclohexamide. The genes are used in the creation of transgenic plants. All of these sequences confer anti-pathogenic properties to transgenic plants. Transgenic expression of 2 or more of the recombinant molecules of the invention that encode anti-pathogenic proteins provides a synergistic increase in plant protection, and may also offer protection against a wider range of pathogens.
                                                                                                                                                                      26-FEB-1998;
27-MAR-1998;
                                                                                                                                                                                                                                       02-SEP-1999.
                                                                                                                                                                                                                                                                                                                               regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; cucumber mosaic virus; ringspot virus; necrosis virus; maize dwarf virus; viroid; bacterial; insect;
                                                                                                                                                                                                                                                                                                                                                                       Zea mays; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY29944 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                        Example 3; Page 73-74; 86pp; English
                                                  New promoter sequences
                                                                                                                   Crane VC
                                                                                                                                                                                                              11-FEB-1999;
                                                                                                                                                                                                                                                                  WO9943819-A1
                                                                                                                                                                                                                                                                                           Zea mays
                                                                                                                                                                                                                                                                                                                      nematode; fungal.
                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays pathogenesis-related class I
                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY29944;
                                                                                                                                            (PION-) PIONEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 ACLLLATILIALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jocal
                                                                            1999-527621/44.
DB; AAZ21207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVGESPY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWVSEKQYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGVFIICSYNPPGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVGVGPVSWDDTVAAYAQSYAAQ-~RQGDCKLIHSG-GPYGENLFWGSAGADWSASDAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
73; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                    98US-0076100
98US-0079648
                                                                                                                                                                                                              99WO-US03011
                                                                                                                                             HI-BRED
                                                                                                                                                                                                                                                                                                                                                                       pathogenesis-related class I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.5%;
                                                  from pathogenesis-related
                                                                                                                                             INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             score 331; DB 16;
Pred. No. 5.6e-23;
1; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                   PR-1#83 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                         PR-1; promoter;
                                                  genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                   of
                                                   maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
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AAZ21186 to

AAZ21190

represents the

nucleotide

sequences

for

promoters

Matches

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (including genes for disease resistance) in plants, especially dicots, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes, particularly enhanced resistance to pathogen-caused disease. Pathogens include viruses such as tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fungi. The present sequence represents a maize PR-1 protein given in the present invention.
The present sequence represents a polypeptide which has antibacterial activity. The antibacterial protein and its polynucleotide can be used for the creation of a plant with resistance against pathogenic microbes " &"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                       (MITU ) MITSUBISHI CHEM CORP.
(BADA) BADAN PENGKAJIAN DAN PENERAPAN TEKNOLOGI.
(BADA) PARKIE BROS.
(BIOI-) BIOINDUSTRY KYOKAI SH.
(DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
                                                                                                                                                                                                                                                                                                                                          02-APR-2002
                                                                                                                                                                                                                                                                                                                                                                       JP2002095477-A
                                                                                                                                                                                                                                                                                                                                                                                                  Elaeis guineensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB77767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB77767 standard;
                                                                    Claim 1; Page 9-10; 13pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of an antibacterial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2002 (first entry)
                                                                                                 New protein and its gene, useful resistance to pathogenic microbes
                                                                                                                                                                                                                                                                                 20-SEP-2000; 2000JP-0285905.
                                                                                                                                                                                                                                                                                                              20-SEP-2000; 2000JP-0285905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 AVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 ACLILATLIALCAAPAPTHGARVIMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCQLIHSG-GPYGENLFWGSAGADWSASDAVG
                                                                                                                                                              2002-439987/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVGESPY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWVSEKQYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGVFIICSYNPPGN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACLLALAMAAIVVAPC------TAQNSPQD-YVDPHNAARA
                                                                                                                                                 ABL59008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 microbe
                                                                       Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 331; DB 20;
Pred. No. 5.6e-23;
1; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance; plant.
                                                                                                       for
                                                                                                                   creating
                                                                                                                   plants with high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
               microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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Best Local
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            25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
06-APR-1999
06-APR-1999
16-APR-1999
21-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
24-MAY-1999
14-MAY-1999
16-MAY-1999
17-MAY-1999
18-MAY-1999
19-MAY-1999
19-MAY-1999
19-MAY-1999
19-MAY-1999
19-MAY-1999
19-MAY-1999
11-MAY-1999
11-MAY-1999
11-MAY-1999
11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188
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              990S-0132484
990S-0132485
990S-0132487
990S-0132487
990S-0134256
990S-0134218
990S-0134211
990S-0134221
990S-0134768
990S-0134768
990S-013494
990S-013495
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99US-0130891.
99US-0131449.
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99US-0130077.
99US-0130449.
                                                                                                                                                                                                                                                                                                                                          99US-0126785.
99US-0127462.
99US-0128234.
99US-0128714.
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Вb ρy Дb QΥ д Qy

40

6

Бр Qy

157 197 97

5-0132048. 5-0132407.

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LCLYNPHGNVQGQSPY 203
                                         EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASY 128
                                                                                        DEVSAHNAARAAVGVGPVSWDNTVAAYAQNYANQ--RIGDCQLVHSG-GPYGENLFWGSG 86
ICNYKPPGNIVGQRPY 162
                                                                                                                                    l Similarity
62; Conserv
                                                                                                                                                                                 162 AA;
                                                                                                                                     Conservative
                                                                                                                                               29.7%;
                                                                                                                                     22;
                                                                                                                                   Score 322; DB Pred. No. 3.8e 22; Mismatches
                                                                                                                                               DB 23;
.8e-22;
                                                                                                                                     48;
                                                                                                                                                          Length 162;
                                                                                                                                     Indels
                                                                                                                                     4;
                                                                                                                                     Gaps
                                                                                                                                     w
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Arabidopsis thaliana. hybridisation assay; genetic termination sequence. Protein identification; signal transduction pathway; metabolic Arabidopsis thaliana protein fragment AAG47493 standard; Protein; entry) 127 mapping; gene expression SEQ ID NO: 59867. pathway;

04-JUN-1999 07-JUN-1999 10-JUN-1999 10-JUN-1999 11-JUN-1999 11-JUN	24-MAY-1999; 25-MAY-1999; 27-MAY-1999; 28-MAY-1999; 01-JUN-1999; 03-JUN-1999;
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standard; Protein; 127 AA.  ;  1000 (first entry)  sis thaliana protein fragment SEQ ID NO: 16101.  sis thaliana protein mapping; geme expression control; promoter; ion sequence.  sis thaliana.  5-A2.  1000; 2000EP-0301439.  1000EP-0301439.  1000EP-030	7		WVAEGRYYTHANNTCAAGROCGTYTQVVWRNTAEVGCAQASCATGAT-LTLCLYNPHGNV 197      :  ::	VGVAPLRNNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRARPAEVVAL 138 	29.1%; Score 315.5; DB 21; Length 127; imilarity 49.2%; Pred. No. 1.1e-21; Conservative 14; Mismatches 47; Indels 3; Gaps 2;	99US-0161992. 99US-0161993. 99US-0162142.
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DB 21; Length

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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an antibacterial protein of Wasabia japonica. The protein can be used in an antibacterial agent and a functional food.
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N-PSDB; ABL59001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 13-14; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-SEP-2000; 2000JP-0284178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibacterial protein gene of Wasabia japonica
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                                                            LLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVG
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l Similarity 48.4%;
61; Conservative 1
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99US-0161992.
99US-0161993.
99US-0162142.
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;; Pred. No. 1.4e-21;
15; Mismatches 47;
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Length 161; Indels

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GYIVSCNYDPPGNVIGKSPY 168
                                                                                                                                                                        EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGANQG
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                                    ATLTLCLYNPHGNVQGQSPY
                                                                                             WASYR-ARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATG 183
                                                                                                                                                    DYLDAHNTARADVGVEPLTWDNGVAAYAQNYASQ-----LAADCNLVHSHGQYGENLA 88
                                                                         WGSGDFLTAAKAVEMWVNEKQYYAHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNG
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31..168
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Pred. No. 1.
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24-MAR-1989;
20-JUN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the sequence of the plant pathogenesis-related protein (PRP), PR-1b. It confers systemic acquired resistance to plants. The corresp. DNA is used in a colimeric construct, to produce transgenic plant cells or tissues with the ability to regenerate into plants which are disease resistant.

See also AAQ06179-80, AAQ06182-86, AAQ06199-Q06208 and AAQ06829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disease-resistant transgenic plants - inducible pathogenesis-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic plants; disease resistance; chimeric plant pathogenesis-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-1991
                                    AAY44003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-313983/42.
N-PSDB; AAQ06181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stinson JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryals JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP392225-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR-1b plant pathogenesis-related
21-DEC-1999
                                                                           AAY44003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 15; page 22; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CIBA ) CIBA
                                                                                                                                                                        118
                                                                                                                                                                                                          183
                                                                                                                                                                                                                                                                                    123
                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                             69 EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN-- 122
                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                            GATLTLCLYNPHGNVQGQSPY
                                                                                                                                                                                                                                                                     QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT 182
                                                                                                                                                                      GGYVVSCNYDPPGNVIGOSPY 138
                                                                                                                                                                                                                                                                                                                          DYLDAHNTARADVGVEPLTWDNGVAAYAQNYVSQ
                                                                                                                                                                                                                                               QGSGDFMT-AAKAVEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVKCNN 117
                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alexander DC,
R, Neuhaus J-M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEIGY AG
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-0425504.
89US-0329018.
89US-0368672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90EP-0105336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodman RM,
Moyer MB;
                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                          203
                                                                           139
                                                                                                                                                                                                                                                                                                                                                                                                 score 303; DB 11;
Pred. No. 1.8e-20;
15; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138
                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   obtd. using encoding a from infected plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meins F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Payne
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB;
                                                                                                                                                                                                                                                                                                                                                                                                     14;
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4.

밁 Qy В δÃ Вþ QΥ

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RESULT 13
AAY44005
ID AAY44
XX AAY44
AC AAY44
AC 21-DE
XX 21-DE
XX Maize
XX Predi
KW Predi
KW homol
KW site
XX Sea m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAV43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for understanding the interaction of a protein with other molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prediction; secondary structure; alignment; evolutionary conservation;
homology; periodicity; co-variation analysis; antigenic site;
site directed mutagenesis; interaction.
      Zea mays
                                          site directed
                                                           Prediction; secondary structure; alignment;
homology; periodicity; co-variation analysis
                                                                                                                    Maize pathogenesis related protein #3
                                                                                                                                                                 21-DEC-1999
                                                                                                                                                                                                         AAY44005;
                                                                                                                                                                                                                                             AAY44005 standard; Protein; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 371-374; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Predicting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-570766/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Benner SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5958784-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tobacco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BENN/) BENNER S
                                                                                                                                                                                                                                                                                                                                               119
                                                                                                                                                                                                                                                                                                                                                                                     183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN-- 122
                                                                                                                                                                                                                                                                                                                                            GGYVVSCNYDPPGNVIGQSPY
                                                                                                                                                                                                                                                                                                                                                                                     GATLTLCLYNPHGNVQGQSPY
                                                                                                                                                                                                                                                                                                                                                                                                                         QGSGDFMT-AAKAVEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVKCNN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGWASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYLDAHNTARADVGVEPLTWDNGVAAYAQNYVSQ-----LAADCNLVHSHGQYGENLA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogenesis related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the folded structure of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                            (first entry)
                                          mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-0857224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-0857224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.9%;
46.1%;
                                                         co-variation analysis; antigenic
                                                                                                                                                                                                                                                                                                                                               139
                                                                                                                                                                                                                                                                                                                                                                                   203
                                          interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 303; DB
Pred. No. 1.8e
L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
1.8e-20;
hes 47;
                                                                              evolutionary conservation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                             site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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AC XXX AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                         06-SEP-2000
                                                                                                 EP1033405-A2
                                                                                                                                                                                                                                                                                                  18-OCT-2000
                                                                                                                                                                                                                                                                                                                                          AAG42365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5958784-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 AA;
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Sequences AAY43902-Y44015 represent proteins used in a novel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites, and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular form using distance constraints imposed by disulfide bridges, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein molecule, as guides for site directed mutagenesis studies, and for
AAG42365 standard; Protein; 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  understanding the interaction of a protein with other molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 375-376; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Predicting the folded structure of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-570766/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 SNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN 122
                                                                                                                                                                                  RDNRGVFIICNYEPRGNIAGMKPY 141
                                                                                                                                                                                                                                                                                                                       IFWGSAGFDWKAVDAVRSWVDEKQWYNYATNSCAAGKVCGHYTQVVWRATTSIGCARVVC
                                                                                                                                                                                                                                                                                                                                                                                        QGW--ASYRARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SENSPQDYLTPQNSARAAVGVGPVTWSTKLQQFAEKYAAQ---RAGDCRLQHSG-GPYGEN 57
                                                                                                                                                                                                                                                   ATG-ATLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0857224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 299; DB 20;
Pred. No. 4.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                           117
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4.

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ESULT 14

AG42365

D AAG42365 standard; Protein; 163 AA.

X

C AAG42365;

T 18-OCT-2000 (first entry)

X Arabidopsis thaliana protein fragment SEQ ID NO: 52828.

X Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; X

X termination sequence.

X Arabidopsis thaliana.

X EP1033405-A2.

X EP1033405-A2.

X 25-FEB-2000; 2000EP-0301439.
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1111111111111			990S-0121825. 990S-0123548. 990S-0125788. 990S-0125785. 990S-0126785. 990S-0128714. 990S-0128714. 990S-013049. 990S-013144. 990S-013144. 990S-01314. 990S-01324. 990S-01324. 990S-01324. 990S-01324. 990S-01324. 990S-01324. 990S-0134.
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14-0CT-1999

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21-0CT-1999

21-0CT-1999
                                                                                                                                                                                                    Transgenic plants; disease resistance; chimeric DNA; plant pathogenesis-related protein.
                        21-MAR-1990;
                                                                  17-OCT-1990
                                                                                                                EP392225-A.
                                                                                                                                                          synthetic.
                                                                                                                                                                                                                                                                 PR-1c plant pathogenesis-related protein.
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17; Mismatches
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24-MAR-1989;
20-JUN-1989;
                                                                                                                                                                                                                             This is the plant pathogenesis-related protein (PRP), PR-1c. It confers systemic acquired resistance to plants. The corresp. DNA is used, in a chimeric construct, to produce transgenic plant cells or -tissues with the ability to regenerate into plants which are disease resistant.

See also AAQ06179-81, AAQ06183-86 and AAQ06199-Q06208.
                                                                                                                                                                                                                                                                                                                                                Disease-resistant transgenic plants - obtd. inducible pathogenesis-related protein from
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                       Example 15; page 22; 77pp; English.
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119
                       184
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                                                                                                    6
GYIVSCNYDPPGNVIGKSPY 138
                      ATLTLCLYNPHGNVQGQSPY 203
                                                  WGSGDFLTAAKAVEMWVNEKQYYAHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNG
                                                                 WASYR-ARPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATG 183
                                                                                                   DYLDAHNTARADVGVEPLTWDDQVAAYAQNYASQ------LAADCNLVHSHGQYGENLA
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Neuhaus J-M,
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89US-0329018.
89US-0368672.
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18; Pred. No. 8.1e-20;
15; Mismatches 51;
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Moyer MB;
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3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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Sequence 100, App
Sequence 45, Appl
Sequence 47, Appl
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Sequence 48, Appl
Sequence 5, Appli
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SULT 2 -07-857-: Sequence Sequence Patent N GENERAL TITLE NUMBE: CORRE: ADD: STR.	197 157	138 97	80 40	20 6	Query Ma Best Loc Matches	SULT 1  -09-257-583 Sequence 13 Sequence 13 GENERAL INF GENERAL INF GENERAL INF CURRENT AF CURRENT AF CURRENT FI NUMBER OF SOFTWARE: SEQ ID NO 1 LENGTH: 1 TYPE: PRI TYPE: CORGANISM: ORGANISM:		28 29 30 30 31 32 33 33 33 44 44 44 44 44 44 44 44 44 44
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224B-102 102, Applicati 0. 5958784 INFORMATION: CANT: Benner, OF INVENTION: R OF SEQUENCES: SPONDENCE ADDRE RESSEE: Steven EET: Hadlaubst	PY 203     PY 163	GRYYTHANNTC 	VAPLRWNAGLAS    :  : : :   VGPVSWDDTVAA	LATLLALCAAPAPTHGA :  :    ALAMAAIVVAPC	ilarit Conse	plica 362 TION: TION: TION: F71 F71 NTION: 1D NC DATIA DATIA DATIA DATIA DATIA TID NC		244.00 244.00 244.00 244.00 244.00 244.00 244.00 244.00 244.00 240.00 240.00
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4B Olded		YTQVVWRNTAEVGC       ::::   YTQVVWRDSTAIGC	GCAFA   DCQLI	RVLMPGGAGAVTKAQQGG	e 331; . No. ismatc	A PR-1 219 57,583	ALIGNMENTS	28882444444444444444444444444444444444
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US-07-857-224B-104; Sequence 104, Application US/07857224B; Patent No. 5958784;
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Matches
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APPLICATION NUMBER: US
FILING DATE: 03/25/92
            CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                                                       APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicti
NUMBER OF SEQUENCES: 114
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DESCRIPTION: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
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MEDIUM TYPE: 3.5 inch diskette, 1.4 mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
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AUTHORS: Carr, J. P.
AUTHORS: Klessig, D. F.
TITLE: Isolation and nucleotide sequence of cDNA clones for
TITLE: pathogenesis related proteins of Nicotiniana tabacum
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Zurich
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Dixon, D. C.
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                                                                         Predicting Folded Structures of Proteins 1114
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46.1%; Pred. No. 3.4e-24;
Live 15; Mismatches 47;
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; VOLUME: 16
; PAGES: 9861
; DATE: 1988
US-07-857-224B-104
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US-07-857-224B-100
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Best Local Similarity
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                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                       APPLICANT: Benner, Steven A TITLE OF INVENTION: Predicti
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                                                                                                                       NUMBER OF SEQUENCES:
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                                                     CITY:
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FILING DATE: 03/25/92
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                                                                                     ADDRESSEE:
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XY: Switzerland
(note: this is an international post code) CH-8092
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Nucleic Acids Research
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Carr, J. P.
Klessig, D. F.
Isolation and nucleotide sequence of cDNA clones for
                                                                   Hadlaubstrasse 151
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pred. No. 9.2e-24;
16; Mismatches 61
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RESULT 5
US-08-181-271A-45
US-08-181-271A-45
; Sequence 45, Application US/08181271A
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CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
                                                                                                                     APPLICANT:
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LENGTH: 138
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TELEPHONE: (International) 41
TELEFAX: (International) 41 1
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DESCRIPTION: protein
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PAGES: 1988
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AUTHORS: Dixon, D. C.
AUTHORS: Carr, J. P.
AUTHORS: Klessig, D. F.
AUTHORS: Klessig, D. F.
TITLE: Isolation and nucleotide sequence of cDNA clones for the
TITLE: pathogenesis related proteins of Nicotiniana tabacum induced by TMV
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FILING DATE: 03/25/92
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ORGANISM: tobacco
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Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
                                               Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                  Duesing, John H. Friedrich, Lesli
                                                                                                                                                  Alexander, Danny C. Beck, James J.
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                                                                                                h, Leslie B.
Robert M.
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262 2437
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FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPHONE: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CHEMICALLY REGULATABLE TITLE OF INVENTION: CHEMICALLY REGULATABLE NUMBER OF SEQUENCES: 106

CORRESPONDENCES: 106
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FILLING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION WITHDEN
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PRIOR APPLICATION NUMBER: US 08/093,301
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APPLICATION NUMBER: US
FILING DATE: 13-JAN-94
                                                                                                                                                         FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                                                                                                                                                                                                    APPLICATION NUMBER: U$ 07/368,672 FILING DATE: 20-JUN-1989 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/305,566
APPLICATION NUMBER: US 07/305,566
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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ADDRESSEE: 7 Skyline Drive
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Ward, Eric
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Stinson, Jeffrey R.
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                                                                                                                                          UMBER: US 08/045,957
12-APR-1993
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                                                            S-19825/P1/CGC 1727
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US-08-449-315-45
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APPLICANT: Ryals, John A.
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SEQUENCE CHARACTERISTICS:
SEQUENCE 168 amino acid
                                                                                                                                                                                                                                                                                        TITLE OF
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                           CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 VALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLTLCLYNPHG 195
                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                        APPLICATION NUMBER: FILING DATE: 24-MAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
FILING DATE:
                APPLICATION NUMBER:
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 LLVSTLLLFLVI---SHSCR-----AQNSQQ------DYLDAHNTARADV 48
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1 Similarity 36.7%;
69; Conservation-
                                                                                                                                                                          10532
                                                                                                                                                                                                                                                                                        INVENTION:
                                                                                                                                                                                                      New York
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                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                  Williams,
                                                                                                                                                                                                                                                                                                                           Uknes, Scott
Ward, Eric R.
                                                                                                                                                                                                                                                                                                                                                           Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                       Payne, George B.
Sperison, Christoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beck, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                      Neuhaus,
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Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Meins, Jr., Frederick
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 13-JAN-94
                                                        24-MAY-1995
                                                                                                                                                                                                                                                                                                                                               Scott J.
                                                                                                                                                                                                                                                                       s, Shericca C.
CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     John H.
                                                                                                                                                                                                                                                                                                                                                                                                    Jean-Marc
               08/181,271
                                                                      US/08/449,315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leslie B.
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Pred. No. 2.6e-22;
Pro. Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (919)541-868! INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 0
APPLICATION NUMBER: US 0
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APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
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APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
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APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                              136 VALWYAEGRYYTHANNTCAAGROCGTYTOVVWRNTAEVGCAQASCATGATLTLCLYNPHG 195
                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/329,018 FILING DATE: 24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-OCT 1989
                                                                                                                                                                82 GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                                                                                                                                                                          13 LLVSTLLLFLVI---SHSCR------AQNSQQ------DYLDAHNTARADV 48
                                                                                                                                                                                                                                                  22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV 81
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Elmer, James REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/042,847 FILING DATE: 6-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                        VEMWYDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG 160
NVQGQSPY 203
                                                                                                                          GVEPLTWDDQVAAYAQNYASQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          James Scott
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16-JUL-1993
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                                                                                                                        -LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
                                                                                                                                                                                                                                                                                                                                    Length 168;
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US-08-444-803-45
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Patent No. 5654414
                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/444,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION MEMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
ADDITCATION MIMBER: US 07/165 667
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APPLICANT:
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Williams, Shericca C. TITLE OF INVENTION: CHEMICALLY REG TITLE OF INVENTION: DNA SEQUENCES NUMBER OF SEQUENCES: 106
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APPLICANT:
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                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 21-DEC-1990
                                                                                                                                                                                APPLICATION NUMBER: US (FILING DATE: 8-MAR-1988 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hawthorne
STATE: New York
                                                                                                                                                 APPLICATION NUMBER: 6-APR-
  APPLICATION NUMBER:
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Stinson, Jeffrey R.
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                                                                                                                                               JMBER: US 08/042,847
6-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mary B.
s, Jean-Marc
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                                                                                                          US 07/632,443
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US 07/848,506
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Best Local S
Matches 69
                                                                                                                                                                                                                                                                                               Sequence 45, Application US/08449043 Patent No. 5689044
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
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APPLICANT:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/329,018
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/100,122, APPLICATION DATA: 27-SEP-1991
PRIOR APPLICATION DATA: US 07/580,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                    APPLICANT:
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APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       196 NVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 VEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LLVSTLLLFLVI---SHSCR------AQNSQQ-------DYLDAHNTARADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 LILATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV
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                                                                                                                                                                                                                                                                                                                                                                                                         NYRGESPY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVEPLTWDDQVAAYAQNYASQ------LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Similarity
                          Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                     Duesing, John H. Friedrich, Leslie Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                             Beck, James J.
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Alexander, Danny C.
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                                                                                                                                                                                          Leslie B.
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PRILING DATE: 6-APR 1993

PRIOR APPLICATION DATA:

APPLICATION UNBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION UNBER: US 07/425,504

FILING DATE: 20-OCT 1989

PRIOR APPLICATION DATA:

APPLICATION UNBER: US 07/848,506

FILING DATE: 6-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION UNBER: US 07/768,122

PRIOR APPLICATION UNBER: US 07/768,122

PRIOR DATE: 27-SEP-1991
                     INFORMATION FOR SEQ ID NO:
                                                        NAME: Elmer, James Scott REGISTRATION NUMBER: 36.129 REFERENCE/DOCKET NUMBER: STELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8614
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EILING DATE: 24-MAX-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:

ON/TOATION NUMBER: 08/181,271
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS_MS_DOS
                                                                                                                                                                                                                                                                                                               PRIOR AFFIGURATION NUMBER: US 0//300/300 FILING DATE: 7-SEP-1990 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/368,672
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        APPLICATION NUMBER: US 07 FILING DATE: 24-MAR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 20-JUN-1989 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                           APPLICATION NUMBER: US 0
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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COUNTRY:
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STREET: 7 Skyline Drive
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                                           (919)541-8689
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
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; TYPE: amino a TOPOLOGY: lin ; MOLECULE TYPE: US-08-449-043-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compate OPERATING SYSTEM: PC-DC SOFTWARE: PatentIn Relaction DATA:
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/181,271
                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                            FILING DATE: 16-JUL-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                    FILING DATE: 13-JAN-PRIOR APPLICATION DATA:
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CITY: Tarrytown
CTATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stinson, Jeffrey R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION. DA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alexander, Dar APPLICANT: Ryals, John A.
                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 VEMMYDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDDPG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 VALWVAEGRYYTHANNTCAAGROCGTYTOVVWRNTAEVGCAOASCATGATLTLCLYNPHG 195
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                                                          FILING DATE:
                                                                                                                                                                      APPLICATION NUMBER: US 07/937,197 FILING DATE: 6-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 GVEPLTWDDQVAAYAQNYASQ~~~~~LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 GYAPIRWNAGIASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 LLVSTLLLFLVI---SHSCR-----AQNSQQ------DYLDAHNTARADV 48
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                                                                                                                APPLICATION NUMBER: US FILING DATE: 1-APR-1991
                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
APPLICATION NUMBER: US 07/165,667 FILING DATE: 8-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                         13-JAN-1994
                                                      UMBER: US 07/305,566
6-FEB-1989
                                                                                                                                                                                                                                   16-JUL-1993
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                                                                                                                                                                                                                                                   US 08/093,301
                                                                                                                                   us 07/678,378
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RESULT 10
US-08-455-416-45
                                                                        Sequence 45, Application US/08455416
Patent No. 5777200
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-JUN-1989
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 07/
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NOTA:
APPLICATION NUMBER: US 08/
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PRIOR APPLICATION NUMBER: US 07/425,504
APPLICATION NUMBER: 20-OCT 1989
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                       APPLICANT:
                                                            APPLICANT:
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APPLICATION NUMBER: 0
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  Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
                                                      Ryals, John A.
Alexander, Danny C.
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
ETILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
ETILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
PILING DATE: 27-SEP-1991
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APPLICANT:
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      FILING LALL.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
PRIOR DATE: 24-MAR-1989
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS: 106
                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US (FILING DATE: 7-SEP-1990)
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    PRIOR APPLICATION DATA
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CITY: F
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/937,197 FILING DATE: 6-NOV-1992
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E: New York
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Stinson, Jeffrey I
Uknes, Scott J.
Ward, Eric R.
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Payne, George B.
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Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goodman,
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N: 800
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Jeffrey R.
                                                                                                                                                      US 07/580,431
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RESULT 11
US-08-455-244-45
; Sequence 45, Application US/08455244
; Patent No. 5789214
• Patent No. PATENTION:
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Best Local Similarity 36.7%;
Matches 69; Conservative 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (919)541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                  APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 VEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 VALMVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLTLCLYNPHG 195
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 GVEPLTWDDQVAAYAQNYASQ------LAADCNLVHSHGQYGENLAEGSGDFWT-AAKA 100
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                                                              COUNTRY:
                                                                                            ADDRESSEE: Clar of Prive
                                                  10532
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amino acid
                                                                            New York
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Payne, George B.
Payne, Christoph
                                                                                                                                                                                                Uknes, Scott ward, Eric R. Williams, She
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Friedrich, Les...
Framan, Robert M.
                                                                USA
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Stinson, Jeffrey R.
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Montoya, Alice
Moyer, Mary B
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Alexander, Danny C.
3: Floppy disk
IBM PC compatible
                                                                                                                         CIBA-GEIGY Corporation
                                                                                                                                                                                                                                     Scott J.
                                                                                                                                                                       CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF
                                                                                                                                                         106
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3; Pred. No. 2.6e-22;
22; Mismatches 59;
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                                                                            Query Match
Best Local Similarity
Matches 69; Conserv
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FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
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PILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
PRIOR APPLICATION NUMBER: US 07/678,378
APPLICATION NUMBER: US 07/678,378
APPLICATION NUMBER: US 07/678,378
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
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PRIOR APPLICATION NUMBER: 08/181,271
APPLICATION NUMBER: 08/181,271
APPLICATION NUMBER: 08/181,271
APPLICATION NUMBER: 08/181,271
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SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08
FILING DATE: 12-APR-1993
ATTORNEY AGENT INFORMATION:
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13 LLVSTLLLFLVI---SHSCR-----AQNSQQ-----
                                   22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV 81
                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                     linear
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20-OCT 1989
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n Release #1.0, Version
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                                                                          %; Score 286; DB 1;
%; Pred. No. 2.6e-22;
22; Mismatches 59;
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  ---DYLDAHNTARADV 48
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US-08-454-876-45
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                         PRIOR APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION NUMBER: US 07/305,566
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION NUMBER: US 07/165,667
APPLICATION NUMBER: US 07/165,667
PRILING DATE: 8-MAR-1988
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION UMBER: 08/181,271
APPLICATION UMBER: 08/181,271
APPLICATION UMBER: 08/181,271
PRICE PAPEL CATEN 13-TANA-04/181,271
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICATION NUMBER: US 01
FILING DATE: 16-JUL-1993
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o. 5804693
               APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uknes,
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Stinson, Jeffrey R.
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Montoya, Alice
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Harms, Christian
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   NUMBER:
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 US 08/042,847
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                                          GENERAL INFORMATION:
APPLICANT: Ryals,
APPLICANT: Alexande
APPLICANT: Beck, Ja
APPLICANT: Duesing,
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APPLICANT:
                                APPLICANT:
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RESULT 13
US-08-457-364-45
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Sequence 45, Application US/08457364
Patent No. 5847258
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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INFORMATION FOR SEQ
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acid
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FILING DATE: 24-MAR-
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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TELEPHONE: (919)541-8614
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TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Elmer, James REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 12-APR-1993
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                                                                                                                                                                                                                                                                                                                           13 LLVSTLLLFLVI---SHSCR------AQNSQQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 7-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                           22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV 81
                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                            NYRGESPY 168
                                                                                                                                            NVQGQSPY 203
                                                                                                                                                                              VEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG
                                                                                                                                                                                                                                                   GVEPLTWDDQVAAYAQNYASQ------LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
                                                                                                                                                                                                                                                                                                                                                                                              69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US 07/329,018
24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US 07/768,122
27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMBER: US 07/425,504
20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                               26.4%;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 286; DB 1;
Pred. No. 2.6e-22;
2; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 168;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                           -DYLDAHNTARADV 48
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Friedrich, Leslie B. Goodman, Robert M. Harms, Christian

Alexander, Danny Beck, James J. Duesing,

a

John H.

Ryals, John A

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APPLICATION NUMBER: 08/1
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 0
FILING DATE: 16-UL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                   FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425 504
FILING DATE: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US FILING DATE: 6-APR-1993 PRIOR APPLICATION DATA:
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                               PRIOR APPLICATION DATA:
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STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01 FILING DATE: 31-MAY-1995 CLASSIFICATION: 800
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US (FILING DATE: 6-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                               APPLICATION NUMBER: US 07/368,672 FILING DATE: 20-JUN-1989
                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 27-SEP-1991
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FILING
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               APPLICATION NUMBER:
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 DATE:
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Sperison, Christoph
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Montoya, Alice
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Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6-NOV-1992
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7-SEP-1990
                                                 MBER: US 07/329,018
24-MAR-1989
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                 US 08/045,957
                                                                                                                                                                                                                      US 07/768,122
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MOLECULE TYPE: protein US-08-457-364-45
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (919)541-861
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE, DOCKET NUMBER: S-T
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 VALMVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLTLCLYNPHG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 GVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LLVSTLLLFLVI---SHSCR-----AQNSQQ------DYLDAHNTARADV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 LLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAV 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                        STREET: 7 Skylin
CITY: Hawthorne
STATE: New York
                                                                                        COUNTRY:
                                                                                                                                       ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEMWVDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVQGQSPY 203
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5851766
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                                                                                                                                                                                                                                                                             Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                          Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
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                                                                                                                                                                                                                                                                                                                                                                                      Harms, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                        Friedrich,
                                                                                                                                                                                                                                                                                                              Payne, George B.
                                                                                                                                                                                                                                                                                                                              Neuhaus,
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                Scott J.
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36.7%;
                                                                                                                                                                                                    CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                        h, Leslie Robert M.
                                                                                                                                                                                                                  CHEMICALLY R
                                                                                                                                                                                                                                                                                                                              Jean-Marc
                                                                                                                                                                                       106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LAADCNLVHSHGQYGENLAEGSGDFMT-AAKA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 286; DB 2;
Pred. No. 2.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-19825/P1/CGC 1727
   Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 168;
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MOLECULE TYPE: protein US-08-456-262-45
                                                                                                                       Query Match 26.4%;
Best Local Similarity 36.7%;
Matches 69; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/165,667
EILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
EILING DATE: 6-APR-1993
PRIOR APPLICATION NUMBER: US 07/632,441
ETILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
ETILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/848,506
ETILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/848,506
ETILING DATE: 6-MAR-1992
PRIOR APPLICATION NUMBER: US 07/768,122
ETILING DATE: 27-SEP-1991
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 07/768,122
ETILING DATE: 27-SEP-1991
                                                                                                                                                                                                                                                                                                       TELEFAX: (919)541-868 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 24-MAR-
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 07/937,197
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                     82
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
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FILING DATE: 31-MAY-1995
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                                                                       GVAPLRWNAGLASAAAGTVAQORRQGGCAFADVGA----SPYGAN--QGWASYRARPAEV 135
                                                  LLVSTLLLFLVI---SHSCR-----AQNSQQ------DYLDAHNTARADV 48
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24-MAR-1989
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eR: S-19825/p1/CGC 1727
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                                                                                                                         Score 286; DB 2; 1
Pred. No. 2.6e-22;
Pred. No. 59;
                                                                                                                                                          Length 168;
                                                                                                                         Indels
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                                                                                                                         Gaps
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US-08-456-240-45
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CITY: New York
TYATE: New York
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 31-MAY-CLASSIFICATION: 800
PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
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                                                  PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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 PRIOR APPLICATION DATA
                                                                                                    FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                 APPLICATION NUMBER: US 08/042,847 FILING DATE: 6-APR-1993
                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/093,301 FILING DATE: 16-JUL-1993
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08,
                                                                                  APPLICATION NUMBER:
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SYSTEM: PC-DOS/MS-DOS
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Floppy disk

31-MAY-1995

08/181,271

US/08/456,240

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8-MAR-1988

us 07/165,667

US 07/305,566

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GENERAL INFORMATION:
                                        NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 VEMWYDEKQYYDHDSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYVVSCNYDPPG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 NYRGESPY 168
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7 Skyline Drive
                                                                                                                                   Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
                                                                                                                                                                                                                                                       Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                         Dues....
Friedrich, Les...
Friedrich, Les...
Friedrich, Les...
                                                                            Williams, Shericca C.
VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
VENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                               Neuhaus, Jean-Ma
Payne, George B.
                                                                                                                                                                                                                                                                                                                                                                                                   Alexander, Danny C. Beck, James J.
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                   CIBA-GEIGY Corporation
                                                                                                                                                                                                                                      Jean-Marc
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PRIOR APPULCATION DATA:

APPLICATION NUMBER: US 07/848,506
ETLING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/768,122
ETLING DATE: 27-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
ETLING DATE: 7-SEP-1990
PRIOR APPLICATION NUMBER: US 07/368,672
ETLING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
ETLING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
ETLING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
ETLING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
ETLING DATE: 12-APR-1993
APPORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 5-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEPAX: (915)541-8689
INFORMATION FOR SED ID NO: 45:
SEQUENCE CHARACTERISTICS:
LEMGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: 11near

MOLECULE TYPE: protein
Search completed: March 19, 2003, 09:37:12 Job time : 16 secs
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EILING DATE: 21-DEC-1990
PRIOR APPLICATION UNMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
                                                                                                     196 NYQGQSPY 203
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161 NYRGESPY 168
                                                                                                                                                                                                                                           136 VALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGATLTLCLYNPHG 195
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Perfect score:
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein -
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length: 2000000000
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Match
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1 MAHSRSHHHLLLLPAPMATA.....ATLTLCLYNPHGNVQGQSPY 203
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Gapop 10.0 ,
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01 US-09-840-479-13
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12 US-10-078-929-86
13 US-10-078-929-84
14 US-10-078-929-96
15 US-10-078-929-96
16 US-10-078-929-96
17 US-10-078-929-97
18 US-10-078-929-97
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Sequence 2, Appli
Sequence 13, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 86, Appl
Sequence 80, Appl
Sequence 81, Appl
Sequence 90, Appl
Sequence 90, Appl
Sequence 90, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appl
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AT AN SG	Matcocal s 2	RESULT 1  US-09-832-320-2  Sequence 2, Application US/098323: Patent No. US20010049834A1  GENERAL INFORMATION: APPLICANT: Crane, Edmund H. APPLICANT: Crane, Virginia C. APPLICANT: Crane, Wirginia C. TITLE OF INVENTION: Maize Pathogs TITLE OF INVENTION: Polynuclect: FILE REFERENCE: 35718/214291  CURRENT APPLICATION NUMBER: US/05  CURRENT FILING DATE: 2001-04-10  PRIOR APPLICATION NUMBER: US 60/1  PRIOR FILING DATE: 2000-04-10  PRIOR FILING DATE: 2000-04-10  NUMBER OF SEQ ID NOS: 3  SOFTWARE: FastSEQ for Windows Verice of Seq ID NOS: 3  SOFTWARE: FastSEQ for Windows Verice of Seq ID NOS: 3  SOFTWARE: FastSEQ for Windows Verice of Seq ID NOS: 3  SOFTWARE: FastSEQ for Windows Verice of Seq ID NOS: 3  LENGTH: 203  TYPE: PRT ORGANISM: Zea mays		193.5 193.5
	nilarity Conser	pplicati pplicati ATION: ATION: Parane, Ed TONION: NATION: NATION: NATION: NATION OF DATE: PER 3571 CE: 35757 CE: 35		17.8 17.8 17.8 17.8 17.8 17.8 17.8 17.8
HHLLLIPADMATACLILA DEYLAPHNOARAAVGVAP LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	100. 100. vative	on US/( 834A1 834A1 Highini Maize I Polyn 8/21422 WJ017 2001 MBER: U MBER: U MBER: U		4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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re 1 SC 1	Length 203; Indels 0; Gaps 0; IGGAGAVTKAOOGGTG 60	Use		Sequence 50, Appl Sequence 47, Appl Sequence 47, Appl Sequence 285, App Sequence 285, App Sequence 285, App

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APPLICANT: Meyers, Blake
APPLICANT: Meyers, Catherine
APPLICANT: Weng, Zude
ITITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
ITITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US Na
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT APPLICATION NUMBER: 09/566,394
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-01
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US-09-840-479-13
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APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 202, Application US/10078929 Patent No. US20020152497A1
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LENGTH: 163
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APPLICANT:
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PRIOR
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CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/257,583
PRIOR FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rafalski, Antoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 VVGESPY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 VQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 LWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 AVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 ACLLLATLLALCAAPAPTHGARVLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
            APPLICATION NUMBER: FILING DATE: 1999-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWVSEKQYYDHDTNSCAEGQVCGHYTQVVWRDSTAIGCARVVCDNNAGVFIICSYNPPGN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCQLIHSG-GPYGENLFWGSAGADWSASDAVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
                                                                                                                                                                                                                                                                                                                                                                                                                            Famodu, Omolayo
Odell, Joan T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Falco, Saveric
Sakai, Hajime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miao, Guo-Hua
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                1999-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saverio Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                             Omolayo O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 331; DB 10;
Pred. No. 3.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TAQNSPQD-YVDPHNAARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
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Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Z
US-10-068-347-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10068347 Patent No. US20020166146A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Maize PR1 Polynucleotides and Methods of Use FILE REFERENCE: 35718/242798 (5718-151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/267,052 PRIOR FILING DATE: 2001-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
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PRIOR FILING DATE: 1999-05-11
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TYPE: PRT
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125
                                                                158 QCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGNVQGQSPY 203
                                                                                                                                                                                                                                                                                                                                42 VLMPGGAGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVA 101
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                                                                                                                                   67 NQ-RAGDCRLVHSG-GPYGENLFWGSAGYAWTASNAVGSWAAEKQYYNHATNTCSAPSGQ 124
                                                                                                                                                                                                                                                                          17 VVAAAAAAGRVVSAQN------TAQDFVNLHNSPRADVGVGNVAWNTTVA-AYAQSYA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 AVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGWASYRA--RPAEVVA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 73; Conserv
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                                                                                                                                                                                                   QQRRQGGCAFADVGASPYGANQGW--ASYRARPAEVVALWVAEGRYYTHANNTCAA--GR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVGESPY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQGQSPY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEVGCAQASCATGA-TLTLCLYNPHGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVGVGPVSWDDTVAAYAQSYAAQ--RQGDCKLIHSG-GPYGENLFWGSAGADWSASDAVG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACLLALAMAATVVAPC-----
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SCGHYTQLVWRASTAIGCARVVCSNNAGVFIICNYYPPGNVIGQSPY
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Acevedo, Pedro
Crane, Virginia
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41.9%;
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Pred. No. 3.7e-21;
1; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Involved

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APPLICANT: Meng, Zude
APPLICANT: Weng, Zude
ITITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
ITITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT APPLICATION NUMBER: US/20/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR APPLICATION NUMBER: 60/133038
PRIOR APPLICATION NUMBER: 60/133042
PRIOR APPLICATION NUMBER: 60/133042
PRIOR APPLICATION NUMBER: 60/133042
PRIOR APPLICATION NUMBER: 60/133042
PRIOR APPLICATION NUMBER: 60/133043
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
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APPLICANT: Famodu, Omora,
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
"PDI,ICANT: Thorpe, Catherine
"PDI,ICANT: Wend, Zude
"""leic Ac
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US-10-078-929-82
                                                                                                                                                                                                                    RESULT 6
US-10-078-929-86
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US-10-078-929-82
                                                                                                                         Sequence 86, Application US/10078929 Patent No. US20020152497A1 GENERAL INFORMATION:
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APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
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      APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio C
APPLICANT: Sakai, Hajime
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                                                                                                                                                                                                                                                                                                                                                 119 WRRSTRIGCARVVCADNRGVFIVCSYDPPGNVNGQRPF 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 AGAVTKAQQGGTGSGSNATADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQG 107
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mes 63; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AAAMAAAMMAATASAQN-TPQDFVNLHNRARAADGVGPVAWDARVARYAQDYAA--KRAG 59
   Miao, Guo-Hua
Falco, Saverio Carl
Sakai, Hajime
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US-10-078-929-86
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PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/13308
PRIOR APPLICATION NUMBER: 60/133042
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR PRIOR DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR APPLICATION NUMBER: 60/133436
PRIOR APPLICATION NUMBER: 60/133436
PRIOR APPLICATION NUMBER: 60/133667
PRIOR APPLICATION NUMBER: 60/137667
PRIOR APPLICATION NUMBER: 60/137667
PRIOR FILING DATE: 1999-06-04
NUMBER: 60/137667
PRIOR FILING DATE: 1999-06-04
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SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
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APPLICANT:
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APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT FALLING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
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APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 NTCDPGKVCGHYTQVVWRXSVRIGCARVVCAANRGVFIT-CNYDPPGNFNGERPF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 NTCAAGRQCGTYTQVVWRNTAEVGCAQASCAT--GATLTLCLINPHGNVQGQSPY 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASFAQSYAA--KRAGDCRLQHSG-GPYGENIFWGSAGRAWSAADAVASWVGEKKNYHYDT
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Falco, Saverio
Sakai, Hajime
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Thorpe, Catherine
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Joan T.
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PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 98

SOFTWARE: Patentin version 3.1

SEQ ID NO 83

LENGTH: 136

TYPE: PRT

ORGANISM: Lycopersicon esculentum
US-10-091-135-83
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TYPE: PRT
; ORGANIZM: Triticum aestivum
US-10-078-929-100
                                                  веst Local
Matches бі
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Matches
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SOFTWARE: Microsoft Office 97
SEQ ID NO 100
                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/091,135
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/272,818
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TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
FILE REFERENCE: 2313/1H587-US1
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PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION UNMBER: 60/137667
PRIOR FILING DATE: 1999-06-04
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OR APPLICATION NUMBER: 60/133038
OR FILING DATE: 1999-05-07
OR APPLICATION NUMBER: 60/133042
OR FILING DATE: 1999-05-07
OR APPLICATION NUMBER: 60/133427
OR FILING DATE: 1999-05-11
OR APPLICATION NUMBER: 60/133437
OR FILING DATE: 1999-05-11
OR APPLICATION NUMBER: 60/133438
OR FILING DATE: 1999-05-11
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69 EYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGAN--QGWA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAF----ADVGASPYGANQGWASYRA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ADAVQANVSEKQYYDHGSNSCSAPADKSCLHYTQVVWRDSTAIGCARVVCDGGDGLFI 151
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                                                       24.6%; Score 267; DB 9; I
Il Similarity 44.2%; Pred. No. 8.2e-16;
61; Conservative 13; Mismatches 54;
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                                                                                              Length 136;
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US-10-078-929-84
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PRIOR APPLICATION NUMBER: 09/566,394
PRIOR APPLICATION NUMBER: 09/13038
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
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SEQ ID NO 84
LENGTH: 164
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APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
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PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
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UNSURE
(140)
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Sakai, Hajime
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TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in TITLE OF INVENTION: Stress Response FILE REFERENCE: BB1357 US NA CURRENT APPLICATION UNMBER: US/10/078,929 CURRENT FILING DATE: 2002-02-19 FRIOR APPLICATION NUMBER: 09/566,394 PRIOR FILING DATE: 2000-05-05 PRIOR APPLICATION NUMBER: 60/133038 PRIOR FILING DATE: 1999-05-07 PRIOR APPLICATION NUMBER: 60/133042 PRIOR FILING DATE: 1999-05-07 PRIOR APPLICATION NUMBER: 60/133427 PRIOR APPLICATION NUMBER: 60/133427 PRIOR APPLICATION NUMBER: 60/133427 PRIOR APPLICATION NUMBER: 60/133427 PRIOR FILING DATE: 1999-05-11 PRIOR APPLICATION NUMBER: 60/133427 PRIOR FILING DATE: 1999-05-11 PRIOR APPLICATION NUMBER: 60/133427 PRIOR PRIOR DATE: 1999-05-11 PRIOR APPLICATION NUMBER: 60/133428 PRIOR PRIOR DATE: 1999-05-11
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; NAME/KEY: UNSURE
; LOCATION: (163)
US-10-078-929-84
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US-10-078-929-96
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SOFTWARE: Microsoft Office 97
SEQ ID NO 96
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-11
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TYPE: PRT
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66 TADEYLAPHNQARAAVGVAPLRWNAGLASAAAGTVAQQRRQGGCAFADVGASPYGANQGW 125
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                                                       Local Similarity les 53; Conserv
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Thorpe, Catherine
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                                                     ; Score 255; DB 12;
; Pred. No. 1e-14;
21; Mismatches 60;
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                                                     60;
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CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
PRIOR FILING DATE: 1999-05-11
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US-10-078-929-90
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TYPE: PRT
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PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-11
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161
                                         174 GCAQASCATGATLTLCLYNPHGNVQGQSPY 203
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                                                                                                                                                                                                                           62 GSNATADEYLAPHNQARAAVGVAPLRWNAGLASAA---AGTVAQQRRQGGC----AFADV 114
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                                                                                                                                                                                                                                                                     vMatch 23.4%; Score 254; DB 12;
Local Similarity 38.7%; Pred. No. 1.5e-14;
Les 58; Conservative 18; Mismatches 60
                                                                                                                   GASPYGANQGWASYRA-RPAEVVALWVAEGRYYTHANNTCAAGRQCGTYTQVVWRNTAEV 173
GCARVVCDDGDVFMTCNYDPVGNYVGERPY 190
                                                                                        GFK-LGENIYWGSGSAWTPSDAVRAWADEEKYYTYATNTCVPGQMCGHYTQIVWKSTRRI 160
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Thorpe, Catherine
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CURRENT EILING LATE: 2002-02-13
PRIOR APPLICATION NUMBER: 02/566,394
PRIOR FILLING DATE: 2000-05-05
PRIOR PELLING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILLING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133427
PRIOR EILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
PRIOR PILLING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
PRIOR PILLING DATE: 1999-05-05-04
NUMBER OF SEO ID NOS: 208
SEOFTWARE: MACROSOFT Office 97
SEO ID NO 94
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US-09-840-479-7
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US-10-078-929-94
Sequence 7, Application US/09840479
Patent No. US20010025380A1
GENERAL INFORMATION:
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
CURRENT APPLICATION NUMBER: US/09/840,479
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/257,583
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APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo O.
APPLICANT: Meyers, Blake
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
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CURRENT FILING DATE: 2002-02-19
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nes 52; Conserv
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Pred. No. 3.4e-14;
1; Mismatches 61;
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; NAME/KEY: UNSURE
; LOCATION: (137)
US-10-078-929-98
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TITILE OF INVENTION: Nucleic Acid Fragments En
TITILE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR PILING DATE: 1909-05-07
PRIOR APPLICATION NUMBER: 60/133036
PRIOR PILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
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Best Local S
Matches 53
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NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
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SEQ ID NO 98
Query Match
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PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
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PRIOR FILING DATE: 1999-05-1
PRIOR APPLICATION NUMBER: 60
PRIOR FILING DATE: 1999-05-1
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PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
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TYPE: PRT
ORGANISM: Zea mays
                                                                                           NAME/KEY: UNSURE LOCATION: (107).
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                                                                                                                                                                         TYPE: PRT
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Thorpe, Catherine
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Pred. No. 1.9e-13;
  Score 240;
  DB
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GENERAL INCORPORATION:
GENERAL INCORPORATION:
APPLICANT: Ploneer Hi Bred International, Inc.
APPLICANT: Simmons, Carl
APPLICANT: Acevedo, Pedro
APPLICANT: Acevedo, Pedro
APPLICANT: Crane, Virginia
TITIE OF INVENTION: Maize PR1 Polynucleotides and Methods of Use
FILE REFERENCE: 35718/242798 (5718-151)
CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/267,052
PRIOR APPLICATION NUMBER: 60/267,052
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 166
TYPE: PRT
CRGANISM: Zea mays
US-10-068-347-2
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US-10-068-347-2
Sequence 2, Application US/10068347
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Search completed: March 19, 2003, 09:41:47 Job time : 17 secs
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                                                                                                                                                                                                             3 GYGGATGKASSGGGGLDPDGDPEVGLNGKAIEEIVNEHNVFRAKEHVPPLVWNATLA--- 59
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February 22, 2003, 04:06:26; Search time 44.5828 Seconds (without alignments) 4209.836 Million cell updates/sec
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/pcrUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/pcrUS_COMB.seq:*
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Search completed: February 22, 2003, 06:08:15 Job tlme : 44.5828 secs

No matches found

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description

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No. Score Match Length DB

Result

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                   March 18, 2003, 14:06:16; Search time 1849 Seconds (without alignments) 7865.629 Million cell updates/sec
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H625654 1007108E	1001114	#601076 BIL 06	86368 525601	26394 PIC1	25875 PIC1	71887 LG1 <u>_</u> 352	W923743 DG1_	67614 PI1_	M322997 PIC1	67270 PI1_'	$1282 6030\overline{1}$	PII	42842 MEST	W746957 WS1 56 C	340658 MEST268-	PIC1 53	678837	M078314 MEST1	072945 MESTS	BG840588 MEST13-F1	E367243 PI1 4	00449 PI1_9	67671 PI1_9	78759 WSI	E367530 PI	97194 PI1_6	M330782 PIO	67638 PI1_9	27258 PIC1	E367670 PI1_9_	67566 PI1 9 D	W678619 WS1	05799 Zea mays	50281 MEST263-	840318 MEST9-A0	873702 MEST9-A0	G840355 MEST12-	337818 MEST217-	Zea II

## ALIGNMENTS

FEATURES source		JOURNAL COMMENT	AUTHORS	REFERENCE	SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 BE512404 LOCUS DEFINITION
Email: walbot@stanford.edu Plate: 946070 row: F column: 05. Location/Qualifiers 1486 /organism="Zea mays"	bepartment of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221	University Unpublished (1999) Contact: Walbot V	Walbot, V.  Walbot, V.  Walbot, V.  Walbot, V.  Walbot, V.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.  1 (bases 1 to 486)	zoi. Zea mays. Zea mays	mays cDNA, mRNA sequence. BE512404 BE512404.1 GI:9733652	HE512404 486 bp mRNA linear EST 07-AUG-2000 946070F05.yl 946 - tassel primordium prepared by Schmidt lab Zea

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RESULT 2
BG343299
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Best Local
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                                                       Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex pre-anthesis spike cDNA library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                            HVSMEg0005F16f, mRNA sequence.
BG343299
BG343299.1 GI:13155628
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                  BG343299 996 bp mRNA linear EST 22-OCT-
HVSMEg0005F16f Hordeum vulgare pre-anthesis spike EST library
HVcDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone
                  Clemson
                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
Clemson
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                                         Contact: Wing RA
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                University Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="0H43"
/db_xref="taxon:4577"
/clone_lib="946 - tas:
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                                          GCCCCGCTGCGGTGGAGCGCGACCTGACGGCGGCGGCGGCGTGGACCGCGTCGCAGCA
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Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop:
Location/Qualifiers
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h quality sequence stop: 717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yellow anther stages (Fenton). Total RNA was prepared from each pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close lab phagemids were plated and picked at the Clemson University (Choi) at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing) Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see https://www.gencome.clemson.edu/nroiects/harley To order
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 310 c 377 g 123 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Hordeum vulgare pre-anthesis spike HVcDNA0008 (white to yellow anther)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
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/lab_host="SOLR"
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/cultivar="Morex"
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Pred. No. 2.1e:
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              GGCCCCGCTGCGGTGGAACGCGGGCCTGCCTTCGGCGGCCGCGCGGGACCGTGGCGCAGCA 370
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1 (bases 1 to 362)

1 (bases 1 to 362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
On Nov 21, 2001 this sequence version replaced gi:1703; Contact: Waugh R, Marshall DF
                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM101325 362 bp mRNA linear EST 23-JUJ EBp101_SQ003_I13_R pistil, 1 DPA, no treatment, cv Optic, EBp: Hordeum vulgare cDNA clone EBp101_SQ003_I13 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                            Seq
                                                                                                                                                                                                                                                                                                                                                                                       Email: est@scri.sari.ac.uk
All sequence has a Phred quality
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                                                                  Conservative
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                                                                                                                            /note="Vector: psport; Site_1: Sal 1; Site_2: Not 1;
Non-normalised library, directionally cloned into psport1.
Derived from pistils dissected from developing grains (24 nours post anthesis) in glasshouse grown barley plants.
Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."

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                                                                                                                                                                                                                                                     /clone="EBP101_SQ003_I13"
/clone_lib="pistil, 1 DPA, no treatment,
/tissue_type="pistil"
/dev_stage="1 DPA"
                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
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                                                                                                                                                                                                                                         /lab_host-"DH10B"
                                                                            32.3%;
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Pred. No. 5.3e-29;
0; Mismatches 45;
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CAGCAGCGGCGGCAGGCGGGTGCGCGTTCGCGGACCTG-GGGGCCAGCCCCTACGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGGCGGCAGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAACCA
                                GCAGGCCGGCAGGGCCGCCGGTCCGGGTTCCCGGACATGAAGCCGGAAGCCCTTACGGCG
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                                                                                                      l Similarity
258; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza.
1 (bases 1 to 681)
1 (bases 1 to 681)
1 (bases 1 to 681)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2017)
Contact: Takuji Sasaki
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
National Institute of Agrobiological 2-1-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki,T. and Yamamoto,K. Rice cDNA from panicle (2 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AU082529 681 bp mRNA linear EST 02-API AU082529 Rice panicle shorter than 3cm Oryza sativa (japonica cultivar-group) cDNA clone E30820, mRNA sequence.
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AU082529
                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 81-298-38-7441
Fax: 81-298-38-7468
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                                                                                                                                                                                             136
                                                                                                        Conservative:
                                                                                                                                                                                       /organism="Oryza sativa (ja
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E30820"
/clone_lib="Rice panicle sl
/dev_stage="shorter than 3d
/note="Organ: panicle"
a 187 c 214 g 141 t
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                                                                                                                       23.1%;
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Pred. No. 1.9e
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CGAACCAGGGGT-GGCAAGCTACCCGGCGCGCGCCCCGCGNAGGTGGTGGCGTCGTGGGTGG

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                                                            CACCCACGCCAACAACACGTGCGCCGCGGGGGGGCAGTGCGGCACGTACACGCAGGTGGT 559
                                                                                                          GCGGCGGTGCGGGTTCGCGGACATGAGCGGGA-CCCCTACGGCGCGAACCAGGGGTGGGC 59
                                                                                                                                        GGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGGC 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCCTACT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACCGGCGCCACGCTCACCATCTGCCTCTACAACCCGCACGGCAACGTGCAGGGCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 293)
Sasaki, T. and Yamamoto, K.
Rice cDNA from immature leaf including apical meristem
Unpublished (1997)
AU029886 293 bp mRNA linear bor utrarr-zov AU029886 Rice cDNA from immature leaf including apical meristem cryza sativa (japonica cultivar-group) cDNA clone E50124_1A, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tsasaki@abr.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Taku
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                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                 /note="Organ: leaf; immature leaf including meristem (under long day condition)" 102 c 107 g 33 t 2 others
                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E50124_lA"
/clone_"E50124_lA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Japan
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                                                                                                                                                                                                                                                                                                  /dev_stage="immature"
                                                                                                                                                                                      19.4%;
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                                                                                                                                                                     Score 174; DB Pred. No. 7.8e 0; Mismatches
                                                                                                                                                                         0;
URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                    Length 293,
                                                                                                                                                                                                                                                                                                                                 leaf including apical
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Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
V., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
, R., Waterston, R. and Wilson, R.
Public Sybban EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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BQ252852

Gm-c1052 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1052-6090 5' similar to SW:ST14_SOLTU Q41495 STS14 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bmail: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Seq primer: -40RP from Gibco
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Location/Qualifiers
                 /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The Harrosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 1 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with the party was constructed in cooperation.
with Dr. Paul Keim's laboratory at Northern Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
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/clone="SOYBEAN CLONE ID: Gm-c1052-6090"
/clone_lib="Gm-c1052"
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/db xref="taxon:3847"
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                                                                                     Coe,E.C.
Direct Submission
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                      Overgo Probes Unpublished (2 2 (bases 1 to
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Zea mays
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Zea mays PCO088779 mRNA
AY106735
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                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 759)
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/note="this sequence is part of a project
assemblies resulting from the application
                                               /organism="Zea mays"
/db_xref="MaizeDB:635032"
/db_xref="taxon:4577"
/clone="PC0088779"
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                                   /clone_lib="Maize Mapping Project/DuPont Cornsensus
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REFERENCE AUTHORS DEFINITION ACCESSION TITLE JOURNAL ORGANISM sequence. BM337818 rt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones unpublished (2001) Individual basecall and Phred software, Tel: 515-294-0975 Fax: 515-294-2299 G405 Agronomy, Schnable Laboratory Contact: Patrick S. Schnable Eukaryota; Viridiplantae; Streptophyta; En Spermatophyta; Magnoliophyta; Liliopsida; Zea mays MEST217-G08.T3 ISUM5-RN Zea mays вм337818 Email: schnable@iastate.edu clade; Panicoideae; Andropogoneae; Zea mays. вм337818.1 (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b 515-294-0975 State University GI:18167978 Iowa State University, confidence value were assigned using 631 bp mRNA linear EST 16-JAN-2002 cDNA clone MEST217-G08 3', mRNA Zea. Ames, Embryophyta; Tracheophyta; a; Poales; Poaceae; PACC ΙA 50011-1010, and USA tissues the

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BASE COUNT
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TGTGGCGCGACTCCACCGCCATCGGCTGTGCCCGCGTCGTCTGCGACAACAACGCCGGCG
                                               TGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCG---CCACGGGCGCCA 615
                                                                                                                                               ACACCCACGCCAACAACACGTGCGCCGCGCGGGCGCAGTGCGGCACGTACACGCAGGTGG 558
                                                                                                                                                                                                     CCGGCGCCGACTGGCGTCCGACGCGTGGGCTCCTGGGTGTCCGAGAAGCAGTACT
                                                                                                                                                                                                                                                     CGAGCTACCGCGCGCGCCGCGCGGAGGTGGTGGCGCTGTTGGGTGGCGGAGGGGGGGTACT 498
                                                                                                                                                                                                                                                                                                                                                                                                               TGTCCTGGGACGACACCGTCGCC----GAGTACGCGCAGAGCTACGCGCGCGCAGCGCCAGG 487
                                                                                                     ACGACCACGACACCAACAGCTGCGCGGAGGGGCCAGGTGTGCGGCCCACTACACGCAGGTGG
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT/TIPPAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mixed"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MEST217-G08"
/clone_lib="ISUM5-RN"
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/cultivar="B73"
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BG840355
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AUTHORS
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JOURNAL
                                                                                                                                                                  Matches 254;
                                                                                                                                                                                               Query Match
                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246
                                                                                               378 CAGGGCGGGTGCGCGTTCGCGGACGTGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGG
                                   166
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                                                               CTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCCGCGGGACGGTGGCGCAGCAGCGGCGG 377
                                  GTGGCGTGGGACGCCAGGGTGGCCAGGTACGCGCAGGACTACGCGGCGAAGCGCGCCGGG
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BG840355.2
EST.
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Zea mays
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Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 bp mRNA linear EST 29-MAY-2001
MEST12-D09.T7-1 ISUM4-TN Zea mays cDNA clone MEST12-D09 5', mRNA
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T7-1 (AA TAC GAC TC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 25, 2001 this sequence version replaced gi:14206677 Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iowa State University
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                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                              ECORI and NotI sites of the PTTTTPAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4577"
/clone="MEST12-D09"
/clone_lib="ISUM4-TN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Zea_mays"
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                                                                                                                                                                  Score 133.8; DB 12;
Pred. No. 8.6e-09;
0; Mismatches 157;
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Zea mays
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BG873702
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BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schnable Laboratory
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Contact: Patrick S. Schnable
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Qiu, F., Cui, F., Guo, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clade; Panicoideae; Andropogoneae;
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515-294-0975
        schnable@iastate.edu
                                                                                                                                                                                                         /clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="PH10B"
                                                                                                                                                                                                                                                               /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGCGCGGGGACGGTGGCGAGCAGCGGCGG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTTCATCGTCTGCAGCTACGACCCCCGGGCAACGTCAACGGCCAGCGCCGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGGCCAGAGCCCCTAC 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTGGCGCAGGTCCACCCGCATCGGCTGCGCGCGCGCGTCGTCTGCGCCGACAACCGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACCACCTGAGCAGCAACACCTGCGACCCCGGCAAGGTGTGCGGCCCACTACACGCAGGTG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCCAGCCCCTACGGCGCGCGAACCAGGGGTGG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGCGTGGGACGCCAGGGTGGCCAGGTACGCGCAGGACTACGCGGCGGAAGCGCCGGG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCGC----CACGGGCGCCC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGGGGCGGCGTGGACGCGCCGACGCGCTGCGTCGTGGGACGAGAAGAGAAGAAGAAGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTGCCGGCTGGTGCACTCGGGGGGGCGGGCCGTTCGGCGAGAACATC---TTCTGGGGGCTCG 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
BG840318
BG840318.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                  Expressed Sequence Tags from Unpublished (2001)
Contact: Patrick S. Schnable
                                                                                                                                                                                FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT, AAC CCT CAC TAA AG)
Seg primer: primer T7-1 (AA TAC GAC TC
                                                                                                                                                                                                                                                                                                                                     Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; Liliopsia clade; Panicoideae; Andropogoneae; Zea.
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MEST9-A05.T7-1 ISUM4-TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                     PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                     F., Cui, F., Guo, L.,
                                                                                                                                                                                                                                                                   515-294-2299
                                                                                                                                                                                                                                                                                    Agronomy, To 515-294-0975
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                                                                                                                                                                                                                                                                                                                    State University
                                                                                                                                                                                                                                                   schnable@iastate.edu
          /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST9-A05"
/clone_lib="ISUM4-TN"
/tissue_type="seedling and silk"
/lab_host="DH10B"
/note="Yector: pT7T3PAC; Site_1: i
   ds-cDNA molecules were
                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                    to 714)
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Pred. No. 8.3e-09;
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2ea mays
pT7T3PAC; Site_1:
les were generated
                                                                                                                                                                                                                                                                                                                                                                                  Ashlock,D.A, Wen,T.J. and Schnable,P.S. from B73 Maize Seedlings and Silks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA linear EST 29-MAY-2001 CDNA clone MEST9-A05 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                     TCA
 EcoRI; Site_2: NotI;
as follows. First-strand
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RESULT 12
BM350281/c
                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                      KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                  JOURNAL
                                                                                                                                                                      TITLE
                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTTCATCGTCTGCAGCTACGACCCCCCGGGCAACGTCAACGGCCAGCGCCCGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
BM350281
BM350281.1
                                                                                          Contact: Patrick S. Schnable Schnable Laboratory
                                                                                                                                Unpublished (2001)
                                                                                                                                            Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones
                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                    Zea
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                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                MEST263-E11
                                                                                                                                                                                                        (bases 1 to 719)
                                                                                                                                                                                                                                                                                    mays
                                                                                                                                                                                                                                                                                                    mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                    515-294-2299
                                    Agronomy, Iowa
515-294-0975
                                                                        State University
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schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA was prepared from oligo-dT selected mRNA by with a NotI oligo-dT primer (5'
                                                                                                                                                                                                                                                                                                                                                                                                  .
T3
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                                                    State University, Ames, IA 50011-1010,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 133.8; DI
Pred. No. 8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157;
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                                                                                                                                                                  and tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                671
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GCGGGGCGCGTGGAGCGCCGCCGACGCGCTGCGGTCGTGGACGAGAAGAGGAAC 

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Best Local Similarity
Matches 254; Conserv
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599
                                                                                                                          GTGGCGTGGGACGCCAGGTGGCCAGGTACGCGCAGGACTACGCGGCGAAGCGCGCCGGG
                                                              CTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCCGCGGGGACGGTGGCGCAGCAGCGGCGG
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conducted using the Lucy software (<a href="http://www.tigr.org/softlabty">http://www.tigr.org/softlabty</a>). Itucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR PRimers
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/clone_lib="ISUM5-RN"
/tissue_type="mixed"
/lab_host="bH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissues: Germinated seed and Seedlings (1, 2, 8, 11 DAG), Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (55 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings,
                                                                                                                                                                                                                                                                                                                                                                                                      resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT713PAC vector. The library then went through one round of normalization to COT value of 5 based on the methods of Marcelo Bento Soares (Genome Research'6: 791-806, 1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-aminocyclopropane-1-carboxylix acid)-treated seedlings, Brassinolide-treated seedlings, RBA (Abscisit acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was molecules were generated as follows.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinetin-treated seedlings, ACPC
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/cultivar="B73"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                        14.9%;
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                                                                                                                                                                                                                                                                        Score 133.8; DB 13; Pred. No. 8e-09;
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                                                                                                                                                                                                                                                    157;
                                                                                                                                                                                                                                                                                                            Length
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Zea mays
AY105799
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whit
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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/db_xref="MaizeDB:638840"
/db_xref="taxon:4577"
/clone="PCO149775"
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An EST database from Sorghum: water-stressed Unpublished (2000)
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Sequences have been tr
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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1 (bases 1 to 539)
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/db_xref="taxon:4558"
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Pred. No. 1.3e-08;
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Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sorghum.
Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,L.H.
An EST database from Sorghum: pathogen-induced plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 539)
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/db_xref="taxon:4558"
/clone_lib="pathogen induced 1 (PI1)"
/clone_lib="pathogen induced leaves from
/note="Organ: Anthracnose-infected leaves from lambda Zap II; Site_l: XhoI;
Vector: pBluescript II from Lambda Zap II; Site_l: XhoI;
Vector: pBluescript II from Lambda Zap II; Site_l: XhoI;
Site_l: ECORI; Two-week-old Sorghum plants (PTX 623
Cultivar) were infected with pathogen (isolate FRM421 of
Cultivar) were infected with pathogen (isolate FRM421 of
Cultivar) were infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
                                 а
                                                                                                                                                                       grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be
                                                                              sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                 pathogen."
173 c 1:
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Search completed: March 18, Job time: 1855 secs

on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
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US-09-257-583-12
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Best Local S
Matches 258
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6.5	6.5	6.6	6.8	6.8	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1
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US-08-459-448A-4	US-07-951-715A-4	US-08-941-936-1	PCT-US96-05611A-12	US-08-487-283A-4	us-09-350-600-10	US-08-971-217-10	US-08-455-736-10	US-08-456-240-10	US-08-456-262-10	US-08-457-364-10	US-08-454-876-10	US-08-455-244-10	US-08-455-416-10	US-08-456-265A-10	US-08-449-043-10	US-08-444-803-10	US-08-449-315-10
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## ALIGNMENTS

Maximum

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; NAME/KEY: CDS
; LOCATION: (92)..(583)
US-09-257-583-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09257583A
Patent No. 6429362
GENERAL INFORMATION:
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 TGTCCTGGGACGACACCGTCGCC---GCGTACGCGCAGAGCTACGCGGCGCAGCGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 TGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGGCGGGGACGGTGGCGCAGCAGCAGCGGCGGC 378
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CGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCCAGAGCCCCTACTAG
                                                                                                                                                                                                                                                                              TGTGGCGCGACTCCACCGCCATCGGCTGTGCCCGCGTCGTCTGCGACAACAACGCCGGCG
                                                                                                                                                                   TGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCAGCTGCG---CCACGGGCGCCA 615
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61.6%;
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Pred. No. 1.7e-16;
0; Mismatches 155;
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; NAME/KEY: CDS
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APPLICANT: Crane, Virginia
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
CURRENT APPLICATION NUMBER: US/09/257,583A
CURRENT FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 37
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SEQ ID NO 6
LENGTH: 866
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                                                                                      GENERAL INFORMATION:
                                                                                                    Sequence 14, Application US/09257583A Patent No. 6429362
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Best Local Similarity
                                          APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes
FILE REFERENCE: 5718-32, 035718/175219
CURRENT APPLICATION NUMBER: US/09/257,583A CURRENT FILING DATE: 1999-02-25 NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
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Pred. No. 3e-
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Best Local
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LENGTH: 80
                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (775)
OTHER INFORMATION: The
OTHER INFORMATION: Or
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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LOCATION: (42)..(686)
498
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hes 254;
                                                     GTGTGGCGCA--ACACCGCCGAGGTCGGGTGCGCGCGAGGCCAGCTGCGC---CACGGGCG
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            CCACGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCAGAGCCCCTAC
                                                                                             GACTGCCGGCTGGTGCACTCGGGGC----GGGCCGTTCGGCGAGAGCATCTTCTGGGGGCTCG
                                                                                                                                                                                           CAGGGCGGGTGCGCGTTCGCGGACGTGGGGGCCCAGCCCCTACGGCGCGCAACCAGGGGTGG
                                        GTGTGGCGCAGGTGTCCACCCGCATCGGCTGCGCGCGTCGTCTGCGCCGACAACCGCG
                                                                                  TACCACCTGAGCAGCAACACCTGCGACCCCGGCAAGGTGTGCGGCCCACTACACGCAGGTG
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US-08-440-856A-9 Sequence 9, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICART: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND
TITLE OF INVENTION: PLANTS WITH S COMPUTER READABLE FORM: NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: CURRENT APPLICATION DATA: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, APPLICATION NUMBER: FILING DATE: 15-MA MEDIUM TYPE: ZIP: COUNTRY: STATE: CITY: WASHINGTON STREET: ADDRESSEE: CLASSIFICATION: 20037 D.C 2000 PENNSYLVANIA AVE. USA MORRISON & FOERSTER Floppy disk 15-MAY-1995 MATERIALS AND METHODS FOR PRODUCING PLANTS WITH SINGLE-SEX FLOWERS A, STEPHEN L. US/08/440,856A Version #1.25

#1

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US-07-945-283-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: US-08-440-856A-9
                                                                                                                                     Sequence 1, Application US/07945283
Patent No. 5355596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
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Best Local
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                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
                                                                                                      TITLE OF INVENTION:
                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 887-1517
                                                                                                                                                                                                                                                                                      588 AACGCGCTGGGCGCCGCCTC 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 CACCAGCCSKYCATGKCGCCSTCKCWCCACGSCTGGGACGGCAATGSCSCCCAMWGSCGYS
             STATE:
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REGISTRATION NUMBER: 36,217
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                              Peoria
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                                                                                                     Pseudorabies Virus Deletion Mutants Involving The EPO and LLT Genes
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Pred. No. 4.6e-05;
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US-07-945-283-1
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Best Local Similarity 49.8%;
Matches 262; Conservative
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                              4214 GTGCTGGAGCCGGACTTGGTGCTGGCGGGGCTGGAGGCCCGGAGCCCGGAGGCCGGAG
                                                                                                                                                                                                                                4038
                                                                                                                                                                 4094
                                                                                                                                                                                                                                                                                       3978 AGCGGCGCTTGCGCCGGGCCCCCGGTCCTCTTCGTCGTCGCGGTGGCCGTGGCCGTCCC 4037
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HYPOTHETICAL: N
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TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19920911
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                   327
                                                                                                                                 267
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STRANDEDNESS: acu
TOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                    GAGTACCTGGCGCCGCACAACCAGGCGCGCGCGCGCGGTGGGCGTGGCCCCGCTGCGGTGG 326
                                                                                                                                                                               CGCGGAGGGCCGAGCCGGAG----AGCCCCTCGTCCTCCTCGCCGTCCCCGGGGGCGGCGCGG 4093
                                                                                                                                                                                                                                                      CGCTCTGCGCCGCGCGGCCGACCCACGGCGCGCGCGCGCTCCTCATGCCGGGCGGCGCGG 207
TGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGGCGAGCTAC 446
                                                              AACGCGGGCCTGGCTTCGGCGGCGCCGCGGGGACGGTGGCGCAGCAGCGGCGGCAGGGCGGG 386
                                                                                              GGGGAGCTGGCGTAGCCGGAGGAGCCGGAGAGCCCGGACTTGGTGCCGGAGCTGGACTTG 4213
                                                                                                                                                           NUCLEIC ACID
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GENERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
TITLE OF INVENTION: MOVEL MOLECULES OF TANGO-77 REI
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION UNMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/094,646
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
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Best Local
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                                                                                                                                                                                                                                                                                                                                                    22264
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LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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560 GTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCTGAGCTGCGCCACGCT 619
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 215; Conserv
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                                                                                                                                                                                                                                                          GCGGTGGAACGCGGGCCTGGCTTCGGCGGCGCCGCGGGACGCTGGCGCAGCAGCAGCGGCA 379
                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 3.0
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nilarity 47.7%;
Conservative
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Pred. No. 0.00039;
0; Mismatches 235
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Patent No. 5
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                                                                                                                                                         APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION NUMBER: US 07/165,667
APPLICATION NUMBER: US 07/165,667
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                                                                                                                                                                                                                                               FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
                                                                                                                                                                                                                                                                                             FILING DATE: 16-JUL-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                       APPLICATION NUMBER: FILING DATE: 21-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 13-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
            APPLICATION NUMBER: US 0 FILING DATE: 20-OCT 1989
                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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Stinson, Jeffrey R.
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Sperison, Christoph
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Meins, Jr., Frederick
Montoya, Alice
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Goodman, Robert M.
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Moyer, Mary B.
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 12-APR-
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5650505
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Moyer,
Neuhaus, Jean ...
Payne, George B.
Payne, Christoph
Parison, Christoph
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                                                                              Meins, Jr., ...
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                                                                                                                                                                                        Alexander, Danny C. Beck, James J.
                                                                     Montoya, Alice
Moyer, Mary B.
                                                                                                                   Harms, Christian
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7-SEP-1990
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56.28;
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APPLICANT: Williams,
TITLE OF INVENTION: OF INVENTION: OF INVENTION: OF INVENTION: I
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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MEDIUM TYPE: Floppy
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                     TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8614
                                                                                                     FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
                                                                     NAME: Elmer, James Scott REGISTRATION NUMBER: 36,
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6-NOV-1992
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> APPLICANT: WAIG, BLIC.
> WILLIAMS, Shericca C.
> WILLIAMS, CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
> VENTION: CHEMICALLY REGULATABLE THEREOF Uknes, Scott J. CIBA-GEIGY Corporation DNA SEQUENCES: 106

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Best Local Similarity 56.2%;
Matches 122; Conservative
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                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                  STREET: 7 Skylin
CITY: Hawthorne
STATE: New York
                                               APPLICATION NUMBER: US/08/444,803 FILING DATE: 19-MAY-1995
                                  CLASSIFICATION:
                                                                                                                                                                                                                                     ADDRESSEE: Cibh Company 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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STRANDEDNESS: single
                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                     10532
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Stinson, Jeffrey R.
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Sperison, Christoph
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Meins, Jr., Frederick
Montoya, Alice
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                                                                                                                                                                                                                                                                CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                               Scott J.
                                                                                                                                                                                                                                                                                                 , Shericea C. CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jean-Marc
08/181,271
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Pred. No. 0.0015;
""amatches 95; Indels
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US-08-444-803-11
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 7-SEP-1 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
FILING DATE: 7-SEP-1990
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APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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APPLICATION NUMBER: US 07/678,378
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-JAN-94
APPLICATION NUMBER: US
FILING DATE: 16-JUL-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Elmer, James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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GTGTTGGATGTGCTAGGGTTCAGTGTAACAATGGAGGATATATTGTCTCTTGCAACTATG 498
                              AGGTCGGGTGCGCGAGGCCAGCTGCGCCACGGGCGCCACGCTCACGCTCTGCCTGTACA 636
                                                                                   CGTGCGCCGCGGGCGGCAGTGCGGCACGTACACGCAGTGGTGTGGCGCAACACACGCCG 576
                                                               CTTGTGCCCAAGGACAGGTGTGTGGACACTATACTCAGGTGGTTTGGCGTAACTCGGTTC 438
                                                                                                                                                                                                  122;
                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                             TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                             696 base pairs
                                                                                                                                                                                                Conservative
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24-MAR-1989
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12-APR-1993
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27-SEP-1991
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                                                                                                                                                                                                                Score 65; DB 1;
Pred. No. 0.0015;
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Patent No. 5
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                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                    FILING DATE: 6-FEB-1989 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US
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                              PRIOR APPLICATION DATA:
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                                            APPLICATION NUMBER: US 0' FILING DATE: 21-DEC-1990
                                                                                                                                      FILING DATE:
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FILING DATE: 13-JAN-94
APPLICATION NUMBER:
FTI.TNG DATE: 20-OCT
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INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
INVENTION: DNA SEQUENCES AND USES THEREOF
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Stinson, Jeffrey R.
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Montoya, Alice
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6-APR-1993
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   US 07/425,504
1989
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                                                                                                                                                                                                                                           Sequence 11, Application US/08456265A Patent No. 5767369
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APPLICANT: Alexan
APPLICANT: Ryals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (919)541-868 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                       APPLICANT:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 CTTGTGCCCAAGGACAGGTGTGTGGACACTATACTCAGGTGGTTTGGCGTAACTCGGTTC 438
                             STREET: 520 Whi
COUNTRY: USA
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                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                    ATCCTCCAGGTAATGTTATAGGCAAAAGCCCATACTA 535
                                                                                                                                                                                                                                                                                                                                                                                     ACCCGCACGGCAACGTGCAGGGCCCAGAGCCCCCTACTA 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 56.:
22; Conservative
                  New York
                                               E: CIBA-GEIGY Corporation 520 White Plains Road, P.O.
                                                                                                               Ryals, JUHH ...
GOOGMAN, ROBERT M.
Stinson, Jeffrey R.
STINSON, CHEMICALLY REGULATABLE
WENTION: CHEMICALLY REGULATABLE
                                                                                                                                                                                        Alexander, Danny C.
Ryals, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (919)541-8614
(919)541-8689
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20-JUN-1989
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56.2%;
                                                                                                      DNA SEQUENCES AND: 111
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Pred. No.
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US-08-456-265A-11
                 Query Match
 Best Local Similarity
                                                                                                                                                       NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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STITING DATE: 7-SEP-1990
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                                                                                       TOPOLOGY:
                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993
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                                                                                                                                         LENGTH:
                                                                                                                                                                                                         TELEPHONE:
                                                                                                                    nucleic acid
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                                                                                                                                                                                         (919)541-8689
                                                                                   linear
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20-OCT 1989
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7.2%;
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Score 65;
Pred. No.
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US-08-455-416-11
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                             PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                             APPLICATION NUMBER: FILING DATE: 6-NOV
                                                                                                                                          FILING DATE: 13-JAN APPLICATION NUMBER:
                                                                                                                                                        APPLICATION NUMBER: 08, APPLICATION NUMBER: 08, APPLICATION DATE: 13-JAN-94
                                                                                                                                                                                                           CLASSIFICATION:
                               APPLICATION NUMBER: US 07/678,378 FILING DATE: 1-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ward, Eric R.
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Stinson, Jeffrey
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Moyer, Mary B
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Payne, George B.
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Meins, Jr., Fred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beck, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ryais,
                                                                                                                                                                                                                                                                                                                                                                                                                              CIBA-GEIGY Corporation
                                                                                                                                                                                                                        31-MAY-1995
                                                                                                                             16-JUL-1993
                                                                               6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       John A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Christoph Jeffrey R.
                                                                                                                                          US 08/093,301
                                                                                                                                                                          08/181,271
 US 07/305,566
                                                                                                                                                                                                                                        US/08/455,416
                                                                                              US 07/937,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leslie B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Frederick
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                                                                                                                                                                                                                                                                          Version
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RESULT 13
US-08-455-244-11
; Sequence 11, Application US/08455244
; Patent NO. 5789214
; GENERAL INFORMATION:
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Best Local Similarity 56.3
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (919)541-868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US FILING DATE: 6-APR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 8-MAR-1 PRIOR APPLICATION DATA:
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LENGTH: 696 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
ANDITOTOR WITHOUT APPLICATION DATA:
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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FILING DATE: 7-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993
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                                                                                                                                                                 ACCCGCACGGCAACGTGCAGGGCCAGAGCCCCTACTA 673
                                                                                                                                                                                                                                                                                                  CGTGCGCGCGGGGCGGCAGTGCGGCACGTACACGCAGGTGGTGTGGCGCAACACACCGCCG 576
                                                                                                                                                                                                                                                                                                                                                                                        CCGCCGAGGTGGTGGCGTGGCGGTGCCGGAGGGGGGGGTACTACACCCACGCCAACAACA 516
                                                                                                                                ATCCTCCAGGTAATGTTATAGGCAAAAGCCCATACTA 535
                                                                                                                                                                                                    GTGTTGGATGTGCTAGGGTTCAGTGTAACAATGGAGGATATATTGTCTCTTGCAACTATG 498
                                                                                                                                                                                                                                        AGGTCGGGTGCGCGAGGCCAGCTGCGCCACGCCCACGCTCACGCTCTGCCTGTACA 636
                                                                                                                                                                                                                                                                               CTTGTGCCCAAGGACAGGTGTGGACACTATACTCAGGTGGTTTGGCGTAACTCGGTTC 438
                                                                                                                                                                                                                                                                                                                                                       CCGCTAAGGCCGTCGAGATGTGGGTCAATGAGAAACAGTATTATGCCCCACGACTCAAACA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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27-SEP-1991
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20-OCT 1989
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-OCT 1989
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APPLICATION NUMBER: US,
FILING DATE: 31-MAY-19
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                           APPLICATION NUMBER: 0-MAR-1992
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
07/768,122
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APPLICATION NUMBER: US (
FILING DATE: 8-MAR-1988
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
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APPLICATION NUMBER: US
FILING DATE: 1-APR-1991
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CORRESPONDENCE ADDRESS:
FILING DATE: 27-SEP-1991 PRIOR APPLICATION DATA:
                                                                                                      APPLICATION NUMBER: FILING DATE: 20-OCT PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/042,847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                             FILING DATE: 6-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/937,197 FILING DATE: 6-NOV-1992
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7 Skyline Drive
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Harms, Christian
Meins, Jr., Freder
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Stinson, Jeffrey R.
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Moyer, Mary B.
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Friedrich,
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Payne, George B.
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Alexander, Danny C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
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FILING DATE: APPLICATION NUMBER:

7-SEP-1990

US 07/580,431

APPLICATION DATA:

US 07/368,672

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Best Local
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APPLICATION NUMBER: US 00
FILING DATE: 12-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
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PRIOR APPLICATION DATA:
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                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                       TITLE OF INVENTION:
                                                                                                        APPLICANT:
                                                                                                                      APPLICANT:
                                                                                                                                       APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 CTTGTGCCCAAGGACAGGTGTGTGGACACTATACTCAGGTGGTTTGGCGTAACTCGGTTC 438
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REGISTRATION NUMBER: 36,
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           STREET:
                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCTCCAGGTAATGTTATAGGCAAAAGCCCATACTA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCCGCACGGCAACGTGCAGGGCCAGAGCCCCTACTA 673
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(919)541-8689
         7 Skyline Drive
                                                      WARDE, FOLK R. WAITH RESIDENCE C. WILLIAMS, Sherica C. WILLIAMS, Sherica C. VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC VENTION: CHEMICALLY REGULATABLE THEREOF
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                                                                                                                                                    Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                 Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                Friedrich, Leslie
Goodman, Robert M.
                                                                                                                                                                                                                                                                                                                                Beck, James J.
                                                                                                                                                                                                                                                                                                                                        Alexander, Danny C.
                                                                                                                                       Uknes,
                                                                                                                                                                                                                                                                 Harms, Christian
                                                                                                                                                                                                                                                                                                              Duesing, John H.
                                                                                                                                                                                    Payne, George B.
                                                                                                                                                                                                      Neuhaus,
                                                                                                                                                                                                                                                 Meins, Jr., Frederick
                                                                                                                                                                                                                                                                                                                                                            Ryals, John A.
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                            CIBA-GEIGY Corporation
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                                                                                                                                       Scott J.
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56.2%;
                                                                                                                                                                                                    Jean-Marc
                                                                                                                                                                                                                                     Alice
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                                                                                                                                                                                                                                                                                               Leslie B.
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Pred. No.
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Query Match
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; MOLECULE TYPE: US-08-454-876-11
                                                                                                                        TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US |
FILING DATE: 1-APR-1991
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/329,018 FILING DATE: 24-MAR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
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APPLICATION NUMBER:
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                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                   FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-JUN-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/632,441 FILING DATE: 21-DEC-1990
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                                                                                                                                                                                                           NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/368,672 FILING DATE: 20-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                  TOPOLOGY:
                                                   STRANDEDNESS:
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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6-MAR-1992
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20-OCT 1989
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Length 696;

US 07/305,566

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APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATI
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                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08
FILING DATE: 13-JAN-94
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ZIP: 10532
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5. 5847258
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New York
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Stinson, Jeffrey R.
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Goodman, Robert M.
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Meins, Jr., Fred
Montoya, Alice
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
DNA SEQUENCES AND USES THEREOF
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Best Local Similarity
Matches 122; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129.
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
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LENGTH: 696 base pairs
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APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
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APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
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APPLICATION NUMBER:
FILING DATE: 7-SEP-1
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FILING DATE: 6-FEB-1
PRIOR APPLICATION DATA:
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499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-OCT 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                         CTTGTGCCCAAGGACAGGTGTGTGGACACTATACTCAGGTGGTTTGGCGTAACTCGGTTC 438
                             ACCCGCACGCCAACGTGCAGGGCCAGAGCCCCTACTA 673
                                                                                                                                                                            CGTGCGCCGCGGGCCCAGTGCGCACGTACACGCAGGTGGTGTGGCGCAACACCGCCG 576
ATCCTCCAGGTAATGTTATAGGCAAAAGCCCATACTA 535
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7-SEP-1990
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6-MAR-1992
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8-MAR-1988
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                                                                                                                                                                                                                                                                                                                                    Score 65; DB 2; Length 696
Pred. No. 0.0015;
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Search completed: March 18, 2003, Job time: 143 secs

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Maximum DB
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//gn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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; PRIOR FILING DATE: 2001
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; LENGTH: 898

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TYPE: DNA
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SULT 1  -09-832-320-1  Sequence 1, Application US/098323  Sequence 1, Application US/098323  Sequence 1, Application US/098323  Sequence 1, Application US/098323  Sequence 1, Application US200100419834A1  GENERAL INFORMATION: Camud H.  APPLICANT: Crane, Edmund H.  APPLICANT: Crane, Virginia C.  TITLE OF INVENTION: Malze Pathog  TITLE OF INVENTION: Malze Pathog  TITLE OF INVENTION: Malze Pathog  TITLE OF INVENTION: MOUNDER: US/0  CURRENT FILING DATE: 2001-04-10  PRIOR APPLICATION NUMBER: US 60/  PRIOR APPLICATION NUMBER: US 60/		60.4	60.4	60.4	50.4	00.	61	61	61	61	61.	61.6	62.6	62.6	62.6	n 0	ο Θ ω	63.4	63.4	64.4	64.6	64.6	66.2	66.2	66.2	
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ULT 1 09-832-320-1 09-832-320-1 equence 1, Application US/09832320 eatent No. US20010049834A1 eneral INFORMATION: ENERAL INFORMATION: Edmund H. APPLICANT: Crane, Edmund H. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Malize Pathogenesis-Related TITLE OF INVENTION: Polynucleotide and Methods of Use FILE REFERENCE: 35718/214291 CURRENT APPLICATION NUMBER: US/09/832,320 PRIOR APPLICATION NUMBER: US 60/195,801	ALIGNMENTS	3-523-	-10-023-5	US-09-976-740-50	US-10-023-523-45	40-4	-4		US-09-894-998-52	US-09-780-717-4	US-09-780-717-6	US-09-772-304A-1	US-09-836-911A-17	US-10-125-767-17	US-09-880-107-3930	US-09-954-456-529	US-09-954-456-292	US-09-976-059-1	US-09-938-842A-2002	US-09-825-288A-1	US-10-101-388-1	0-101-388-2	-10-023-52	S-10-023-529-	US-09-976-740-48	
		50,	Sequence 50, Appl		4	Sequence 45, Appl	48	49	χ.	- :	Sequence 6, Appli	Seguence 1 Appli	Sequence 17. Appr	Sequence 17 Appl	sequence 3950, Ap	Sequence 529, App	Sequence 292, App		Sequence 2002, Ap	1,	Sequence 1, Appli	2, A	App	e 4	Sequence 48, Appl	

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; LOCATION: (63)...(674)
US-09-832-320-1
                                                                                                                        Query Match
Best Local Similarity 100.
Matches 898; Conservative
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                                                  CAATGGCGCACTCGCGCAGCCACCACCACCTCCTCCTGCTCCCGGGGCCCATGGCCACGG
CTCGCACGCACTCGACGCTCATTCACTGAGCCATTTACTCAGATCACCAACTCCAGATCT
                                                                                                                         100.0%; Si
100.0%; P
ative 0;
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Pred. No. 3.1e-152;
; Mismatches 0;
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Sequence 3, Application US/09832320

Patent No. US20010049834A1

GENERAL INFORMATION:
APPLICANT: Crane, Edmund H.
APPLICANT: Crane, Virginia C.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Pathogenesis-Related
TITLE OF INVENTION: Polynucleotide and Methods of
FILE REFERENCE: 35718/214291
CURRENT APPLICATION NUMBER: US/09/832,320
CURRENT APPLICATION NUMBER: US 60/195,801
PRIOR FILING DATE: 2000-04-10

NUMBER OF SED ID NOS: 3
SEQ ID NOS: 3
LENGTH: 612
TYPE: DNA
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(612)
-09-832-320-3
                                             ORGANISM: Zea
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                   ; NAME/KEY: CDS
; LOCATION: (92)..(583)
US-09-840-479-12
                                                                                                                                                                                                                                                         US-09-840-479-12
                                                                                                                                                                                                                     Sequence 12, Application US/09840479 Patent No. US20010025380A1 GENERAL INFORMATION:
                                                                                       NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 12
LENGTH: 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 612; Conserv
                                                                                                                                                             TITLE OF INVENTION: Family Of Maize PR-1 Genes FILE REFERENCE: 5718-92, 035718/175219
CURRENT APPLICATION NUMBER: US/09/840,479
CURRENT FILING DATE: 2001-04-23
                                                                                                                                       PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1999-02-25
                                                                                                                                                                                                             APPLICANT: Crane, Virginia
                                                      TYPE: DNA
ORGANISM: Zea
FEATURE:
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Pred. No. 3.7e-101;
Score 139;
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Query Match

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Local Similarity

Conservative

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Pred. No. 1.3e-16;
0; Mismatches 155;

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US-09-840-479-6
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Patent No. US20010025380A1
GENERAL INFORMATION:
APPLICANT: Crane, Virginia
                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.4
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Crane, Virginia
TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
FILE REFERENCE: 5718-32, 035718/175219
CURRENT APPLICATION NUMBER: US/09/840,479
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/257,583
PRIOR APPLICATION NUMBER: 09/257,583
PRIOR FILING DATE: 1999-02-25
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                      FEATURE:
145
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                                                                                                        TGTCGTGGGATGAGAACGTGGCCGCCCTTCGCGCGGAGCTACGCCGCGCAGCGCCAGGGCG
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Pred. No. 2.4e-16;
0; Mismatches 154;
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (760)
US-10-078-929-81
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US-10-078-929-81
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PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
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LENGTH: 783
                  Query Match
Best Local Similarity
   Matches
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acid Fragments TITLE OF INVENTION: Stress Response FILE REFERENCE: BB1357 US NA
                                                                                                                                                                                                                 SOFTWARE: Microsoft Office
                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-11
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/133438 PRIOR FILING DATE: 1999-05-11
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APPLICANT: Miao, Guo-Hua
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                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
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Thorpe, Catherine
Weng, Zude
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Sakai, Hajime
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     Conservative
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                     13.6%;
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   0;
                    Score 121.8;
Pred. No. 1.6
   Mismatches 157;
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                  1.6e-13;
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US-09-840-479-14
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Matches 254
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SEQ ID NO 14
LENGTH: 806
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APPLICANT: Crane, Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Family Of Maize PR-1 Genes FILE REFERENCE: 5718-32, 035718/175219
CURRENT APPLICATION NUMBER: US/09/840,479
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 09/257,583
PRIOR FILING DATE: 1999-02-25
NUMBER OF SEQ. ID NOS: 37
                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                   NAME/KEY: unsure LOCATION: (775)
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                           LOCATION: (42)..(686)
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nes 254; Conserv
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            GTGTGGCGCAGGTGTCCACCCGCATCGGCTGCGCGCGTCGTCTGCGCCGACAACCGCG
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 Conservative
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Pred. No. 1.6e-13;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)
US-10-068-347-3
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Best Local Similarity
Matches 258; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/267,052
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Simmons, Carl
APPLICANT: Acevedo, Pedro
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Maize PR1 Polynucleotides
FILE REFERENCE: 35718/242798 (5718-151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 772
TYPE: DNA
ORGANISM: Zea 1
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 TACTAGCTAGCT
                              GCCGGCGTCTTCATCATCTGCAACTATTACCCGCCGGGCAACGTGATTGGACAGAGCCCT
                                              GGCGCACGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGGCCAGAGCCCC
                                                                                         CAGCTGGTGTGGCGCCCTCCACTGCCATCGGATGCGCCCGCGTCGTCTGCAGCAACAAC
                                                                                                         CAGGTGGTGTGGCGCAACACCGCCGAGGTCGGGTGCGCGC---AGGCCAGCTGCGCCACG
                                                                                                                                                 TACAACCACGCCACCAACACCTGCTCCGCTCCGTCCGGCCAGTCGTGCGGCCACTACACG
                                                                                                                                                                                                          GCGGGCTACGCCTGGACGCGTCGAACGCCGTGGGATCCTGGGCGGCGGAGAAGCAGTAC
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; ORGANISM: Oryza sativa
US-10-078-929-85
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LENGTH: 714
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
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PRIOR ETLING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/
PRIOR EILING DATE: 1999-05-07
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NUMBER OF SEQ ID NOS: 208
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FILING DATE: 1999-05-11
APPLICATION NUMBER: 60/
FILING DATE: 1999-05-11
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                  CCAGGGGTGGGCGAGCTACCGCGCGCGCGCGCGCGAGGTGGTGGCGGTGGGGTGGCGGA 487
                                                                                                                                                CGTGGCCCCGCTGCGTGGAACGCGGGGCCTGGCTTCGGCGGCGCGCGGGGACGGTGGCGCA 367
                                                          GCGCGCCGGCGACTGCCGGCTGCAGCACTCCGGCGGGCCGTACGGCGAGAACATCTT---
                                                                                      GCAGCGGCGGCAGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAA 427
                                                                                                                    CGTCGGCCCGGTGAGCTGGGACCCCAAGGTCGCCAGCTTCGCGCAGAGCTACGCGGCCAA
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Odell, Joan T.
Meyers, Blake
Thorpe, Catherine
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70; Conservative
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Sakai, Hajime
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Pred. No. 9.4e-13;
0; Mismatches 211;
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; TYPE: DNA
; ORGANIZM: Triticum aestivum
US-10-078-929-99
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US-10-078-929-99
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Best Local Similarity
                                                                                                                                                                                                                                               SOFTWARE: Microsoft Office SEQ ID NO 99
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PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/078, CURRENT FILING DATE: 2002-02-19 PRIOR APPLICATION NUMBER: 09/566,394 PRIOR FILING DATE: 2000-05-05
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-11
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142
                           319 TGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGGCGGCGGGACGGTGGCGCAGCAGCGGCGGC 378
                                                                                         CCCCTAC
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Thorpe, Catherine
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Odell, Joan T.
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Sakai, Hajime
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56.9%;
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                                                                                                                                    Score 108.6; DB Pred. No. 3.4e-11
                                                                                                                         Mismatches
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Sequence 9, Application US/10068347
Patent NO. US20020166146A1
GENERAL INFORMATION:
APPLICANT: Pioneer Hi-Bred International, Inc.
APPLICANT: Simmons, Carl
APPLICANT: Simmons, Carl
APPLICANT: Acevedo, Pedro
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Maize PRI Polynucleotides and
FILE REFERENCE: 35718/242798 (5718-151)
CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/267,052
PRIOR FILING DATE: 2001-02-07
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; LOCATION: (1)..(285)
US-10-068-347-9
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: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 9
: LENGTH: 525
: TYPE: DNA
: ORGANISM: Zea mays
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US-10-068-347-9
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Best Local 9
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                                                CGCCACGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCAGAGCCCCCTA 670
                                                                                                CCAGATCGTGTGGCGACGCACCACCGCCGTCGGCTGCGCCCCGGGTGGCGTGCGACGGCGG
                                                                                                                     GCAGGTGGTGTGGCGCAACACCGCCGAGGTCGGGTGCGCCCAGGCCAGCTGCGCCACGGG
                                                                                                                                                                CGCCGACTACTCGTACGCCGACAACGCGTGCGCGCAGGCCGGGAGTGCGCGCACTACAC
CTAGCTAGCTGAGGTCATCAGGTCGTAGCGACGG
                                                                                                                                                                                     GGGCGGGCCCGGCGCGCCCCGGGACGCCGTCGCGGACTGGGCCGCCGAGGG 101
                               CGGGGTGTTCATCACCTGCAACTACTACCCGCCCGGCAACGTCGTCGGCGAGAGGCCGTA 281
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170; Conservative
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Pred. No. 5.1e-11;
0; Mismatches 104;
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; NAME/KEY: unsure
; LOCATION: (547)
US-10-078-929-97
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                                                                                                                                Query Match
Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 97
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PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
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CURRENT FILING DATE: 2002-02-19
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APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio
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PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
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TITLE OF INVENTION: Nucleic Acid Fragments
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
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                                                             APPLICATION NUMBER:
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Thorpe, Catherine
Weng, Zude
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Odell, Joan T.
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Pred. No. 2.6e-09;
0; Mismatches 172
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US-10-078-929-83
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PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133437
PRIOR APPLICATION NUMBER: 60/133438
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                                                                                                                                                                            NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office
SEQ ID NO 83
LENGTH: 534
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TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
                                   TYPE: DNA
ORGANISM: OLYZA S.
FEATURE:
FEATURE:
LOCATION: (94)
NAME/KEY: unsure
LOCATION: (178)
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PRIOR APPLICATION NUMBER: 60/
PRIOR APPLICATION NUMBER: 60/
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-05-11
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Odell, Joan T.
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APPLICANT: Pioneer Hi-Bred International, Inc.
APPLICANT: Simmons, Carl
APPLICANT: Simmons, Carl
APPLICANT: Acevedo, Pedro
APPLICANT: Crane, Virginia
TITLE OF INVENTION: Maize PRI Polynucleotides and Met
FILE REFERENCE: 35718,242798 (5718-151)
CURRENT APPLICATION NUMBER: US/10/068,347
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION WHEER: 60/267,052
PRIOR FILING DATE: 2001-02-07
                                                                                                                                               RESULT 13
US-10-068-347-1
Sequence 1, Application US,
Sequence 1, Sequence 10, US20020166146A1
Patent No. US20020166146A1
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Matches 259; Conserv
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Pred. No. 1.3e-08;
0; Mismatches 221;
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version
SEQ ID NO 1

3.0

LENGTH:

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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-938-842A-1676
; Sequence 1676, Application
; Patent No. US20020160378A1
                                                          US-09-938-842A-1676
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; LOCATION: (1)..(501)
US-10-068-347-1
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity 51.3
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                            APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                       TYPE: DNA
ORGANISM: Arabidopsis
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ORGANISM: Zea mays
                                                                                                              LENGTH: 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 CATCATCATGTGCAGCTACTGGCCGCCGGGGAACTACCACGGCGTTAAGCCATACTA 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 GCCGATCGAGGAGATCGTGAACGAGCACAACGTGTTCCGCGCCAAGGAGCACGTGCCTCC 152
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 72.2;
No. 0
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US-10-095-407-16/c
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                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 215; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 16
LENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Pan, Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/10095407 Patent No. US20020164330A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/095,407
CURRENT FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/091,650
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/054,646
PRIOR FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL MOLECULES OF TITLE OF INVENTION: AND USES THEREOFFILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 18
                                                                 22204
                                                                                                                                 ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                320
                                                                                                  261
                                                                                                                                                                  201 GGCGCGGGCGGTGACCAAGGCGCAGCAGGGTGGCACCGGCAGCGGCAGCAACGCGACG
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                                                                                  GCGGTGGAACGCGGGCCTGGCTTCGGCGGCGCCGCGGGGACGGTGGCGCAGCAGCGGCGGCA 379
                                                               GCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCGCCACGGGCGCCACGCTCACGC
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Pred. No. 0.00079;
0; Mismatches 235;
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Search completed: March 18, 2003, 16:30:06 Job time: 180 secs

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Result
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Maximum DB seq length: 2000000000
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Maximum Match 100%
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
            898
612
140.6
139
137.6
121.8
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1: /SIDS2/gcgdata/g
2: /SIDS2/gcgdata/g
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24: /SIDS2/gcgdata/
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68.2
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15.5
15.3
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11.7
9.5
9.3
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Matches 898;
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    This sequence represents the DNA sequence PR-1mz. This sequence was isolated by scr
                                                                                              New DNA contg. plant systemic acquired resistance genes - and transgenic plants contg. them, impart disease and pest resistance. also Arabidopsis gene promoter to control DNA transcription
                                                                    Claim
                                                                                                                                                                                                                                                    Alexander DC,
                                                                                                                                                                                                                                                                                          (CIBA ) CIBA
                                                                                                                                                                                                                                                                                                                                   13-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                          03-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maize; PR-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAR; tobacco;
                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR-1 like gene PR-1mz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ99804 standard;
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DB; AAR91595.
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acquired reistance response; anti-pathogen; plant protection;
                                                                Page 70; 85pp;
                                                                                                                                                                                                                                                                                          GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS.
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  sequence
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                       of a
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  maize PR-1 like
ng a BTH-induced
gene,
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Best Local s
Matches 259
                                                                                                                                       regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; cucumber mosaic virus; ringspot virus; necrosis virus; maize dwarf virus; viroid; bacterial; insect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library of maize. The library was screened using a probe matching to the PR-1 barley clone HVPR1BR. This sequence, AAQ99800-Q99803 and AAQ99805 are all used in recombinant/chimaeric DNA molecules of the invention. These sequences were isolated by differential screening of cDNA library, followed by analysis by Northern hybridisation to RNA in the presence and absence of cyclohexamide. The genes are used in the creation of transgenic plants. All of these sequences confer anti-pathogenic properties to transgenic plants. Transgenic expression of 2 or more of the recombinant molecules of the invention that encode anti-pathogenic proteins provides a synergistic increase in plant protection, and may also offer protection against a wider range of
                                                                                                       Zea mays
                                                                                                                                 nematode;
                                                                                                                                                                                      Zea mays;
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                                                                                                                                                                                                                                                                                               AAZ21207 standard;
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                                                                                                                                                                                                                                                                                                                                                                                              616
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hes 259;
                                                                                                                                                                                                             mays pathogenesis-related class I PR-1#83 gene.
                                                                                                                                                                                                                                                                                                                                                                            CGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAAGGCCCAGAGCCCCTACTAG
                                                                                                                                                                                                                                                                                                                                                                                                               TGTGGCGCGACCTCCACCGCCATCGGCTGTGCCCGCGTCTGCGACAACAACGCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                TGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAAGGCCAGCTGCG---CCACGGGCGCCA
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                                                                                                                                                                                   maize; pathogenesis-related class
                                                                                                                               fungal; ss.
                                                                                                                                                                                                                                        (first entry)
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                 /product= "PR-1#83"
/note= "path~~~
                                                               Location/Qualifiers
92..583
                                                                                                                                                                                                                                                                                               DNA;
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                     "pathogenesis-related
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                                                                                                                                                                                   I; PR-1;
                     class
                                                                                                                                                                                  promoter;
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W09943819-A1

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RESULT 5
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ID AAZ:
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AC AAZ:
XX
AC 22-1
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (including genes for disease resistance) in plants, especially dicots, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes, the genetic manipulation of plants to exhibit specific phenotypes, particularly enhanced resistance to pathogen-caused disease. Pathogens include viruses such as tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fungi. The present sequence encodes a maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-527621/44.
P-PSDB; AAY29944.
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27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New promoter sequences from pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PION-) PIONEER HI-BRED INT
   22-NOV-1999
                     AAZ21191;
                                        AAZ21191
                                                                                                                                                                                                                                                                                                                                    345
                                                                                                                                                                                                                                                                                                       319
                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                      protein given in the present invention.
                                                                                        TCTTCATCATCTGCAGCTACAACCCGCCGGGCAACGTCGTCGGCGAGAGCCCCTACTAG
                                                                                                                                         TGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCG----CCACGGGCGCCCA
                                                                                                                                                                              CCGGCGCCGACTGGCTCCGACGCCGTGGGCTCCTGGGTGTCCGAGAAGCAGTACT
                                                                                                                                                                                                                           GCGACTGCCAGCTGATCCACTCCGGCGGGCCCTACGGCGAGAACCTCTTCTGGGGCTCCG
                                                                                                                                                                                                                                                                AGGGCGGGTGCGCGTTCGCGGACGTGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGG
                                                                                                                                                                                                                                                                                    TGTCCTGGGACGACACCGTCGCC---GCGTACGCGCAGAGCTACGCGGCGCAGCGCCAGG
                                                                                                                                                                                                                                                                                               TGCGGTGGAACGCGGGCCTGGCTTCGGCGGCGCGCGGGGACGGTGGCGCAGCAGCAGCGGCGGC
                                                                                                          CGCTCACGCTCTGCCTGTACAACCCGCACGGCAACGTGCAGGGCCCAGAGCCCCTACTAG
                                                                                                                              TGTGGCGCGACTCCACCGCCATCGGCTGTGCCCGGGTCGTCTGCGACAACAACGCCGGCG
                                                                                                                                                                    ACGACCACGACACCAACAGCTGCGCGGAGGGGGCAGGTGTGCGGCCACTACACGCAGGTGG
                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     749
                                        standard;
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     BP;
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98US-0079648
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                                                                                                                                                                                                                                                                                                                                                                                                    160
                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                       15.5%;
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Pred. No. 1
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1.8e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Crane VC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1998;
27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-SEP-1999
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PION-) PIONEER
                                                                                                                                                   145
             496
                                                                                          379
                                                                                                                               319
                                325
                                                   439
                                                                       265
                                                                                                            205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mays
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Zea mays; maize; pathogenesis-related class I; PR-1; promoter; regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; cucumber mosaic virus; ringspot virus; necrosis virus; maize dwarf virus; viroid; bacterial; insect;
Claim 22; Page 65-66; 86pp; English.
                                          New promoter sequences from pathogenesis-related genes
                                                                                                                1999-527621/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathogenesis-related
                                                                                                                                                                                                                                                   98US-0076100.
98US-0079648.
                                                                                                                                                                                                                                                                                                                      99WO-US03011
                                                                                                                                                                                                        HI-BRED INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
111.581
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "PR-1#52"
                                                                                                                                                                                                          INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 class I PR-1#52
                                                                                                                                                                                                                                                                                                                                                                                                                                                         class I protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                  of maize
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AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (including genes for disease resistance) in plants, especially dicots, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes, particularly enhanced resistance to pathogen-caused disease. Pathogens include viruses such as tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fingi. The present sequence encodes a maize PR-1 protein given in the present invention.

Sequence 866 BP; 213 A; 228 C; 240 G; 185 T; 0 other;

Destrocal Similarity 62.4%; Pred. No. 3e-12;
Matches 267; Conservative 0; Mismatches 154; Indels 7; G

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TGTCGTGGGATGAGAACGTGGCCGCCCTTCGCGCGGAGCTACGCCGCGCAGCGCCAGGGCG ACTACACCCACGCCAACAACACGTGCGCCGCGGGGGCGGCAGTGCGGCACGTACACGCAGG GCGGCGGCAGCGCCTGGAAGGCGTCGGACGCCGTCGGCTTGTGGGGTGGGGGAGAAGCAGA CGAGCTACCGCGC---GCGCCCCGCGAGGTGGTGGCGCTGTGGGTGGCGGAGGGGCGGT ACTGCAAGCTGGTGCACTCCGGCGGCGGGCCCAACCACTACGGGGAGAACATCTTCTGGG AGGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGG TGCGGTGGAACGCGGGCCTGGCTTCGGCGGCCGCGGGGACGGTGGCGCAGCAGCAGCGGCGC Conservative 0; Gaps 384 438 378 318 555 495 324 264 204

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                                                                              AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (including genes for disease resistance) in plants, especially dicots, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes,
                       particularly enhanced resistance to pathogen-caused disease. Pathoge include viruses such as tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fungi. The present sequence encodes a maize PR-1 protein given in the present invention.
                                                                                                                                                                                                                                                                Crane
                                                                                                                                                                             Claim
                                                                                                                                                                                                     New
                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                         (PION-) PIONEER
                                                                                                                                                                                                                                                                                                                26-FEB-1998;
27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                     11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                             02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                    W09943819-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nematode;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays; maize; pathogenesis-related class I; PR-1; promoter; regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; consaic virus; consaic virus; ringspot virus; necrosis virus; maize dwarf virus; viroid; bacterial; insect;
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                                                                                                                                                                                                   promoter sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mays
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DB; AAY29943.
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                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGTCTGGCGCAA-ATCCCCGCCATCGGCTGCGCCCGCGTCGTCTGCAACAACGGCGGTG
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                                                                                                                                                                           Page 74-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fungal; ss.
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98US-0079648.
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/product= "PR-1#93"
/note= "pathogenesi
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Sequence 806

B₽;

158

Α;

243 c;

260 G;

144 T;

1 other;

Claim 3;

Page 8-9; 13pp; Japanese

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RESULT 7
ABL59008
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Best Local Similarity
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               New protein resistance t
                                                                                                                                                                                                                    CDS
                                           P-PSDB;
                                                                                              (MITU ) MITSUBISHI CHEM CORP.
(BADA-) BADAN PENGKAJIAN DAN PENERAPAN TEKNOLOGI.
                                                                                                                           20-SEP-2000; 2000JP-0285905
                                                                                                                                             20-SEP-2000;
                                                                                                                                                               02-APR-2002
                                                                                                                                                                                 JP2002095477-A.
                                                                                                                                                                                                                                            Elaeis guineensis.
                                                                                                                                                                                                                                                              Antibacterial protein; microbe resistance;
                                                                                                                                                                                                                                                                                Nucleotide sequence of an antibacterial protein.
                                                                                                                                                                                                                                                                                                    20-AUG-2002
                                                                                                                                                                                                                                                                                                                      ABL59008;
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DB; ABB77767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACCACCTGAGCAGCAACACCTGCGACCCCGGCAAGGTGTGCGGCCACTACACGCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGTCTTCATCGTCTGCAGCTACGACCCCCCGGGCAACGTCAACGGCCAGCGCCCGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTGCCGGCTGGTGCACTCGGGC----GGGCCGTTCGGCGAGAGCATCTTCTGGGGGCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254;
                                                                      DOKURITSU GYOSEI HOJIN
                                                                              PT PAKRIE BROS.
BIOINDUSTRY KYOKAI SH
                                                                                                                                                                                                                                                                                                                                      standard; DNA; 846
               and its gene,
to pathogenic
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                                                                                                                                            2000JP-0285905
                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                          Location/Qualifiers
35..523
/*tag= a
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/product= "antibacterial
                                                                                                                                                                                                                                                                                                  entry)
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                 microbes
                        useful
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                                                                      SANGYO
                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                       creating plants with
                                                                     GIJUTSU
                                                                                                                                                                                                protein'
                                                                                                                                                                                                                                                              plant;
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Best Local S
Matches 245
25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a polypeptide which has antibacterial activity. The antibacterial protein and its polynucleotide can be used for the creation of a plant with resistance against pathogenic microbes
                                                                                                                                                                                                     Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss
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                                                                                                                                                                                                                                                                                                                                   AAC49084 standard;
                                                                                                                              06-SEP-2000
                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                         Arabidopsis
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                                                                                                                                                                                                                                                                                                         AAC49084;
                                                                                                     25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                               AGGTCATCAGGTCGTAG
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                                                                                                                                                                                                                                                         thaliana DNA fragment SEQ
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                                                                                                     2000EP-0301439
 990S-0121825.
990S-0123180.
990S-0123548.
990S-01235788.
990S-0126264.
990S-0126785.
990S-0127462.
                                                                                                                                                                                                                                                                                                                                   DNA;
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56.1%;
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Best Local Similarity 53.0%;
Matches 233; Conservative
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Pred. No. 0.00019;
0; Mismatches 198;
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Matches 232
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04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
08-OCT-1999;
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20-SEP-1999;
22-SEP-1999;
444 AAACCTTTCTACAATTATAAGTCAGACACGTGTGCTGCGAACCACACGTGCGGGGTTTAT
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31-AUG-1999;
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3-OCT-1999;
          GGGCGGTACTACACCCACGCCAACAACACGTGCGCCGCGGGGGCGGCAGTGCGCACGTAC
                                                                                    CGGCAGGCCGGGTGCGCGTTCGCGGACCTGGGGGCCCAGCCCCTACGGCGCGAACCAGGGG
                                                                                                                           CCGCTGCGGTGGAACGCGGGCCTGGCTTCGGCGGCCGCGGGGACGGTGGCGCAGCAGCGG
                                                  TGGGCGAGCTACCG-----CGCGCGCCCCCGCCGAGGTGGCGCGCTGTGGGTGGCGGAG
                                                                       AACCAAAAGAAGTGTGAGTTCGCGAGTCTAAACCCTGGAAAATACGGCGCGAACCAGCTT
                                                                                                          CCACTAGTTTGGAGCCAGACGTTGGAAGCTGCTGCGAGTCGGTTGGCTCGTTACCAGAGG
                                   TGGGCTAAGGGCTTAGTAGCCGTGACACCGTCTCTTGCTGGAGACTTGGGTGAAGGAG
                                                                                                                                                                                     232;
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990S-0161360.
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9908-0154018

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Pred. No. 0.00032;
0; Mismatches 199;
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RESULT 10
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                                                                                                                                    The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides oligonucleotides (specifically AAX55180-271) can be used for the
                                             antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, respiratory distress syndrome, pain, cystic fibrosis, pulmonary whometension unlmonary useconstriction.
         pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronobstructive pulmonary disease (COPD), and cancers such as leukemias,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; paln; cystic fibrosis;
pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
 lymphomas, carcinomas e.g. colon cancer, breast
                                                                                                                                                                                                                                                                                                                               Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                      vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                 New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9913886-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense oligonucleotide; multiple target; antisense treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTCAACGGTGTTGACCATTTGTTTTTACAATCCTCCTGGAAATATAATTGGCCAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGCCAC----GCTCACGCTCTGCCTGTACAACCCCGCACGGCCAACGTGCAGGGGCCAGGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACAAGTCGTCTGGAGAAACTCTAAAGAGCTCGGGTGTGCTCAAGCCACGTGTACGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGCAGGTGGTGTGGCGCAACACCGCCGAGGTCGGGTGCGCGCAAGCCAGCTGCGCCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAST CAROLINA
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97US-0059160
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cancer,
                                  chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          665
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RESULT 11
AAX53491
ID AAX53
XX AAX53
XX AAX53
XX AAX53
XX D5-JU
D7 05-JU
D7 05-JU
D7 05-JU
D8 Humar
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                                                                                                                                                                                                                                                                                                                                                                 104198 NNHNNNSGCCCGGCCCGACNNHNNNSGCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 114955 BP;
                pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
                                                                                                                                                              Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                                                                                          AAX53491 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153
 colon cancer;
                                                    acute asthma; allergy; asthma;
respiratory distress syndrome;
                                                                                        pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                  05-JUL-1999
                                                                                                         impaired respiration; inflammation;
                                                                                                                            Antisense oligonucleotide; multiple target; antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GECCYGCGCNNHNNNSGGCGGCGCGCCCYGGCCYGCGGNNHNNNSCGGCGCGCGCCCCYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCVGGCCVGCGGNNHNNNSCGGCGCGCCCVG-GCCVGCGGNNHNNNSGCGGCGCGCCCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSCCCGGCCGGCGCGCCCCVGGCCVGCGGNNHNNNSGCCCGGCCGGCGGCGCCCCVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCGCGCCCVGGCCVGCGGNNHNNNSCCGGCCGGCGGCGCCCVGGCCVGCCGGNNHNN 104379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCYGCGGNNHNNNSGGCCCGGCCGGCGCGCCCCYGCCGNNHNNNSCGGCCCG
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                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                          DNA;
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                                                                                                                                                                                                                                                                          114955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 83.4;
Pred. No. 0.
                                                    impeded respiration;
pain; cystic fibrosis;
                                                                                                                                                                                                                                                                          ВP
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                                                                                                           lung disease;
                                                                                                                                                                                                                                                                                                                                                                   104166
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   cancer;
                                                                                                                              treatment;
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lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize

metastasized to the lungs, including breast and prostate cancer.

21328 T;

21427 other;

Length 114955;

Sequence 114955 BP; 6071 A; 29417 C; 36712 G;

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The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 1'-rend, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target oligonucleotides (specifically AAX55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and
                                                                                       inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, imprespiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronobstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. golon cancer, breast cancer, lung cancer, lymphomas, carcinomas e.g. golon cancer, breast cancer, lung cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-1998;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense oligonucleotides used vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYEC-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAST CAROLINA
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97US-0059160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment
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                                                                                                                            emphysema, chronic
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밁 망 QΥ 밁 Qy Ş 밁 Qy δÃ Query Match Best Local ( Matches 104783 104723 104903 104843 104963 121181 241 301 Local Similarity hes 212; Conserv BGGGCGCGSNNNDNNCCGCBGGCCBGGGCGSNNNDNNCCGCBGGCCBGGCGSNNNDNN 104782 GGGCGCGCCGGCCGGGCCGSNNNDNNGCBGGCCBGGGCGCGCCGGCCGGCCGG CGGTGGCCTGCCCTGCGGTGGAACGCCGGGCCTGGCTTCGGCGGCCGCGGGGACGG CCGCBGGCCBGSNNNDNNCCGCBGGCCBSNNNDNNCCGCBGGCCSNNNDNNCGCBGGCCB CCGCBGGCCBGGGCSNNNDNNCCGCBGGCCBGGCSNNNDNNCCGCBGGCCBGGSNNNDNN NNNDNNCBGGCCBGGGCGCCGCCGGCCGGCCGSNNNDNNBGGCCBGGGCGCGCCGCC -----TGGCGCAGCAGCGGCGGCAGGCGGGTGCGCGTTCGCGGACGTGGGGGGCCAGC Conservative 9.1%; 66; Score 81.6; DB 20; Pred. No. 0.00051; Mismatches 335; Indels 7; Gaps 180 413 104902 104842 240 360 105022 104962 1;

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99US-0130449. 99US-0130510. 99US-0130891. 99US-0131449. 99US-0132407. 99US-0132484. 99US-0132485. 99US-0132486. 99US-0132487. 99US-0132487. 99US-0132487. 99US-0134218. 99US-0134218. 99US-0134218. 99US-0134219. 99US-0134270.	99US-0121825. 99US-0123180. 99US-012548. 99US-012578. 99US-0126264. 99US-012626. 99US-012626. 99US-012824. 99US-012824. 99US-012824. 99US-012824. 99US-012874.	oter; te	dard; DNA; (first ent haliana DN assay; ge		GCCGGCCGGCCGSNNNDNNGGCCBGGCGCGCCGCCGGCCGGCCGGCCGSNNNDNNGCCBGGGCG 105082  CTGTGGGTGGCGGAGGGGCGGTACTACACCCACGCCAACAACACGTGCGCGGGGGGGG
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990S-0144335 990S-0144632 990S-0144814 990S-0145086 990S-0145086 990S-0145087 990S-0145089 990S-0145089 990S-014518 990S-014518 990S-0145216 990S-0145216 990S-0145216 990S-0145216 990S-0145218	. – – – – – – – – – – – –		, , , , , , , , , , , , , , , , , , , ,		

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RESULT 13
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ID ABL59
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Best Local S
Matches 207
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26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                              Antibacterial
                                                                                                                                                                                                                Nucleotide
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       P-PSDB; ABB77766
                 WPI; 2002-439986/47
                                                      19-SEP-2000; 2000JP-0284178
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                                                                                                                                                                                                                                                                                                                                                                                             384
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Local Similarity 50.6%;
hes 207; Conservative
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990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
990S-0162142.
                                                                                                                                                                                              protein; antibacterial agent; food;
                                                                                                                                      Location/Qualifiers
34.522
/*tag= a
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/product= "antibacterial protein"
                                                                                                                                                                                                                 an antibacterial protein.
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                        misc_feature
                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                         Pseudorabies virus; PRV; LLV; large latency transcript; attenuated virus; vaccine; early protein 0; EPO; HSV-1 ICPO; protecting animals; deletion mutants; swine; ds.
                                                                      TATA_signal
                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding Pseudorabies virus large latency transcript
                                                                                                                                                                                                                                                                                                                                                       Pseudorabies virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ73500 standard; DNA; 8438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibacterial protein gene of Wasabia japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 GGCTCATACACTCTGGTG------GTTCTTACGGCGAGAACTTGGCATGGGGAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 AAGACTATCTAAGGGTTCACAACCAGGCACGAGCGGCGGTAGGCGTTGGCCCCATGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCCTTCGAACACGTGCAACGGAGTT-----TGTGGTCACTACACTCAGGTTGTTTGGA
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                                                                                       predicted
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                                                                                                                                                           PRV strain
                                                                                                                                                                                                                                PRV strain
                                                                                       amino acid sequence of ORF2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC AAQ73500 shows the Pseudorabies virus (PRV) large latency transcript CC (LLT). The basic sequence is derived from PRV strain InFh and PRV CC strain Ka. The LLT overlaps and is transcribed in the opposite CC orientation with respect to the EPO (early polypeptide 0) and the CC immediately early gene (IE180). EPO is nonessential for replicatio, CC LLT is the only gene expressed during PRV latency, and the IE180 cC gene is absolutely necessary for PRV replication. However there are CC of the IE180 copies is viable. Deletions in the non-overlapping cC regions of IE180 repense while senes which have a reduced ability to reactivate from latency. This CC mutants. The invention is concerned with the construction of attennated CC viruses which have a reduced ability to reactivate from latency. This CC can be achieved by functionally disabling the expression of the EPO canoral and amendation.
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                   4274
                                                                                                                                                                                                           4094
                                                                                                                                                                                                                                                                   4038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ73501 and AAR60620-24)
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                                                   TGCGCGTTCGCGGACCTGGGGGGCCAGCCCCTACGGCGCGAACCCAGGGGTGGGCCAGCTAC
                             GGGGCGCCCGCCGCCGCGCGCCGCGCGCTGGGACGACGACGCCGGCCTGCTCGGGCCAG
                                                                                     GTGCTGGAGCCGGACTTGGTGCTGGCGGGGCTGGAGGGCCCGGAGCCCGGGAGGCCGGAG
                                                                                                                                                                         GAGTACCTGGCGCGCACACCAGGCGCGCGCGCGGCGGTGGGCGTGGCCCCCGCTGCGGTGG
                                                                                                                                                                                                      GCCCCGGGCGCGCGCTTCTTCTTGCGCCGCTCGGGCGCGCTGGGTCCGGGCCGGCGCG
                                                                                                                                                                                                                          GCGCGGTGACCAAGGCGCAGCAGGGTG-GCACCGGCAGCCAGCAAGCCAACGCGACGGCGAC
                                                                                                                                                                                                                                                                                          AACGCGGGCCTGGCCTTCGGCGGCGCCGCGGGGACGGTGGCGCAGCAGCAGCGGCAGGCGGG
                                                                                                                                              GGGGAGCTGGCGTAGCCGGAGGAGCCGGAGAGGCCGGACTTGGTGCCGGAGCTGGACTTG
                                                                                                                                                                                                                                                               AGCGGCGCTTGCGCCGGGGCCCCCGGTCCTTCGTCGTCGCCGGTGGCCGTGGCCGTCCC 4037
                                                                                                                                                                                                                                                                                                                                                                                    262;
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8382..8387
                                                                                                                                                                                                                                                                                                                                                                                               7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43pp;
                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                Score 70.4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        3327 G; 1054 T;
                                                                                                                                                                                                                                                                                                                                                                      J. 026;
256;
                                                                                                                                                                                                                                                                                                                                                                                                           DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 8438;
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RESULT 15
ABQ40858
ID ABQ40
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                                                                                        This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-cpc-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucletides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to two CC classes of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of cell carge of the central nervous, cardiovascular, gastrointestinal and respiratory completes setc., particularly by detecting mutations or single nucleotide conjumorphisms (SNP's); and (ii) for differentiation of cell or tissue cethylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the central for the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ40858 standard; DNA; 712 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2001; 2001WO-EP10074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200218632-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for detecting cytosine methylation SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-371829/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGCCCCGGCCACGTTGGCCGGGGCGAAGAGGGCCGCGGGCGTAGGTCCAGGCGGCCTCG 4453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACGCCAACAACACGTGCGCCGCGGGGGCGCAGTGCGGCACGTACACGCAGGTGGTGTGG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCAACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCGCCACGG 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                             of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG
                                                                             invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guetig
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                                                                                                                                                                                                    GGCGCGGTGACCAAGGCGCAGCAGGGTGGCACCGGCAGCGACGCGACGGCGAC
                                                                                 CGCGCGCGCCCGAGGTGGTGGCGCTGTGGGTGGCGGAGGGGCGGTACTACACCCAC
                                                                                                                   TGCGCGTTCGCGGACGTGGGGGCCAGCCCCTACGGCGCGAACCAGGGGTGGGCGAGCTAC
                                                                                                                                            AACACCGCCGAGGTCGGGTGCGCGCAGGCCAGCTGCGCCACGGGCGCCACGCTCACGCTC
                                                GCCAACAACACGTGCGCCGCGGGGGGCAGTGCGGCACGTACACGCAGGTGGTGTGGCGC 566
                                                                                                  GAGTACCTGGCGCGCACAACCAGGCGCGCGCGGCGGTGGGCGTGGCCCCGCTGCGGTGG
                                  Conservative
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                                                                                                                                                                                                                                                                               Score 70;
Pred. No.
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                0.034;
                                                                                                                                                                                                                                                                                      DB 24; Length 712;
                                                                                                                                                                                                                                                                        252;
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Job time : 374 secs Search completed: March 18, 2003, 14:12:18